ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-α (TNF-α) EXPRESSION

INTRODUCTION

This application is a continuation of U.S. Application Serial No. 09/824,322, filed April 2, 2001, which is a continuation-in part of U.S. Application Serial No. 09/313,932, filed May 18, 1999 (U.S. Patent 6,228,642), which is a continuation-in-part of U. S. Application Serial No. 09/166,186 filed October 5, 1998 (U.S. Patent No. 6,080,580).

FIELD OF THE INVENTION

This invention relates to compositions and methods for modulating expression of the human tumor necrosis factor-α (TNF-α) gene, which encodes a naturally present cytokine involved in regulation of immune function and implicated in infectious and inflammatory disease. This invention is also directed to methods for inhibiting TNF-α mediated immune responses; these methods can be used diagnostically or therapeutically. Furthermore, this invention is directed to treatment of conditions associated with expression of the human TNF-α gene.

BACKGROUND OF THE INVENTION

Tumor necrosis factor α (TNF-α also cachectin) is an important cytokine that plays a role in host defense. The cytokine is produced primarily in macrophages and monocytes in response to infection, invasion, injury, or inflammation. Some examples of inducers of TNF-α include bacterial endotoxins, bacteria, viruses, lipopolysaccharide (LPS) and cytokines including GM-CSF, IL-1, IL-2 and IFN-γ.

TNF-α interacts with two different receptors, TNF receptor I (TNFRI, p55) and TNFRII (p75), in order to

transduce its effects, the net result of which is altered gene expression. Cellular factors induced by TNF-α include interleukin-1 (IL-1), interleukin-6 (IL-6), interleukin-8 (IL-8), interferon-γ (IFN-γ), platelet derived growth factor (PDGF) and epidermal growth factor (EGF), and endothelial cell adhesion molecules including endothelial leukocyte adhesion molecule 1 (ELAM-1), intercellular adhesion molecule-1 (ICAM-1) and vascular cell adhesion molecule-1 (VCAM-1) (Tracey, K.J., et al., Annu. Rev. Cell Biol., **1993**, *9*, 317-343; Arvin, B., et al., Ann. NY Acad. Sci., **1995**, *765*, 62-71).

Despite the protective effects of the cytokine, overexpression of TNF-α often results in disease states, particularly in infectious, inflammatory and autoimmune diseases. This process may involve the apoptotic pathways (Ksontini, R., et al., J. Immunol., **1998**, *160*, 4082-4089). High levels of plasma TNF-α have been found in infectious diseases such as sepsis syndrome, bacterial meningitis, cerebral malaria, and AIDS; autoimmune diseases such as rheumatoid arthritis, inflammatory bowel disease (including Crohn's disease), sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant (allograft) rejection; and organ failure conditions such as adult respiratory distress syndrome, congestive heart failure, acute liver failure and myocardial infarction (Eigler,A., et al., Immunol. Today, **1997**, *18*, 487-492). Other diseases in which TNF-α is involved include asthma (Shah,A., et al., Clinical and Experimental Allergy, **1995**, *25*, 1038-1044), brain injury following ischemia (Arvin,B., et al., Ann. NY Acad. Sci., **1995**, *765*, 62-71), non-insulin-dependent diabetes mellitus (Hotamisligil et al., Science, **1993**, *259*, 87-90), insulin-dependent diabetes mellitus (Yang et al., *J. Exp. Med.*, **1994**, *180*, 995-1004), hepatitis (Ksontini et al., J. Immunol., **1998**, *160*, 4082-4089), atopic dermatitis (Sumimoto et al., Arch.

Dis. Child., **1992**, *67*, 277-279), and pancreatitis (Norman et al., Surgery, **1996**, *120*, 515-521). Further, inhibitors of TNF-α have been suggested to be useful for cancer prevention (Suganuma et al. (*Cancer Res.*, **1996**, *56*, 3711-3715). Elevated TNF-α expression may also play a role in obesity (Kern, *J. Nutr.*, **1997**, *127*, 1917S-1922S). TNF-α was found to be expressed in human adipocytes and increased expression, in general, correlated with obesity.

There are currently several approaches to inhibiting TNF-α expression. Approaches used to treat rheumatoid arthritis include a chimeric anti-TNF-α antibody, a humanized monoclonal anti-TNF-α antibody, and recombinant human soluble TNF-α receptor (Camussi, *Drugs*, **1998**, *55*, 613-620). Other examples are indirect TNF-α inhibitors including phosphodiesterase inhibitors (e.g., pentoxifylline) and metalloprotease inhibitors (Eigler et al., Immunol. Today, **1997**, *18*, 487-492). An additional class of direct TNF-α inhibitors is oligonucleotides, including triplex-forming oligonucleotides, ribozymes, and antisense oligonucleotides. Several publications describe the use of oligonucleotides targeting TNF-α by non-antisense mechanisms. U.S. Patent 5,650,316, WO 95/33493 and Aggarwal et al. (*Cancer Research*, **1996**, *56*, 5156-5164) disclose triplex-forming oligonucleotides targeting TNF-α. WO 95/32628 discloses triplex-forming oligonucleotides especially those possessing one or more stretches of guanosine residues capable of forming secondary structure. WO 94/10301 discloses ribozyme compounds active against TNF-α mRNA. WO 95/23225 discloses enzymatic nucleic acid molecules active against TNF-α mRNA.

A number of publications have described the use of antisense oligonucleotides targeting nucleic acids encoding TNF-α. The TNF-α gene has four exons and three introns. WO 93/09813 discloses TNF-α antisense oligonucleotides conjugated to a radioactive moiety, including sequences targeted to the 5'-UTR, AUG start site, exon 1, and exon 4 including the stop

codon of human TNF-α. EP 0 414 607 B1 discloses antisense oligonucleotides targeting the AUG start codon of human TNF-α. WO 95/00103 claims antisense oligonucleotides to human TNF-α including sequences targeted to exon 1 including the AUG start site. Hartmann et al. (*Mol. Med.*, **1996**, *2*, 429-438) disclose uniform phosphorothioates and mixed backbone phosphorothioate/phosphodiester oligonucleotides targeted to the AUG start site of human TNF-α. Hartmann et al. (*Antisense Nucleic Acid Drug Devel.*, **1996**, *6*, 291-299) disclose antisense phosphorothioate oligonucleotides targeted to the AUG start site, the exon 1/intron 1 junction, and exon 4 of human TNF-α. d'Hellencourt et al. (*Biochim. Biophys. Acta*, **1996**, *1317*, 168-174) designed and tested a series of unmodified oligonucleotides targeted to the 5'-UTR, and exon 1, including the AUG start site, of human TNF-α. Additionally, one oligonucleotide each was targeted to exon 4 and the 3'-UTR of human TNF-α and one oligonucleotide was targeted to the AUG start site of mouse TNF-α. Rojanasakul et al. (*J. Biol. Chem.*, **1997**, *272*, 3910-3914) disclose an antisense phosphorothioate oligonucleotide targeted to the AUG start site of mouse TNF-α. Taylor et al. (*J. Biol. Chem.*, **1996**, *271*, 17445-17452 and *Antisense Nucleic Acid Drug Devel.*, **1998**, *8*, 199-205) disclose morpholino, methyl-morpholino, phosphodiester and phosphorothioate oligonucleotides targeted to the 5'-UTR and AUG start codon of mouse TNF-α. Tu et al. (*J. Biol. Chem.*, **1998**, *273*, 25125-25131) designed and tested 42 phosphorothioate oligonucleotides targeting sequences throughout the rat TNF-α gene.

Interestingly, some phosphorothioate oligodeoxynucleotides have been found to enhance lipopolysaccharide-stimulated TNF-α synthesis up to four fold due to nonspecific immunostimulatory effects (Hartmann et al. *Mol. Med.*, **1996**, *2*, 429-438).

Accordingly, there remains an unmet need for therapeutic compositions and methods for inhibiting expression of TNF-α, and disease processes associated therewith.

SUMMARY OF THE INVENTION

The present invention provides oligonucleotides which are targeted to nucleic acids encoding TNF-α and are capable of modulating TNF-α expression. The present invention also provides chimeric oligonucleotides targeted to nucleic acids encoding human TNF-α. The oligonucleotides of the invention are believed to be useful both diagnostically and therapeutically, and are believed to be particularly useful in the methods of the present invention.

The present invention also comprises methods of modulating the expression of human TNF-α in cells and tissues using the oligonucleotides of the invention. Methods of inhibiting TNF-α expression are provided; these methods are believed to be useful both therapeutically and diagnostically. These methods are also useful as tools, for example, for detecting and determining the role of TNF-α in various cell functions and physiological processes and conditions and for diagnosing conditions associated with expression of TNF-α.

The present invention also comprises methods for diagnosing and treating infectious and inflammatory diseases, particularly diabetes, rheumatoid arthritis, Crohn's disease, pancreatitis, multiple sclerosis, atopic dermatitis and hepatitis using the oligonucleotides of the present invention. These methods are believed to be useful, for example, in diagnosing TNF-α-associated disease progression. These methods are believed to be useful both therapeutically, including prophylactically, and as clinical research and diagnostic tools.

One embodiment of the present invention is a method of treating an inflammatory disorder in an individual comprising administering to said individual an effective amount of an

oligonucleotide up to 30 nucleotides in length complementary to a nucleic acid molecule encoding human tumor necrosis factor-α, wherein the oligonucleotide inhibits the expression of said human tumor necrosis factor-α and comprises at least an 8 nucleobase portion of SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 34, SEQ ID NO: 39, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 149, SEQ ID NO: 157, SEQ ID NO: 264, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 290, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 315, SEQ ID NO: 334, SEQ ID NO: 418, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 431, SEQ ID NO: 432, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 494 or SEQ ID NO: 496. Preferably, the antisense oligonucleotide is administered orally. In one aspect of this preferred embodiment, the inflammatory disorder is inflammatory bowel disease, Crohn's disease, colitis or rheumatoid arthritis. Preferably, the oligonucleotide comprises at least one modified intersugar linkage. Preferably, the modified intersugar linkage is a phosphorothioate or methylene(methylimino) intersugar linkage. In another aspect of this preferred embodiment, the oligonucleotide comprises at least one 2'-O-methoxyethyl modification. Preferably, the oligonucleotide comprises at least one 5-methyl cytidine. In one aspect of this preferred embodiment, every cytidine residue is a 5-methyl cytidine.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-B are graphs showing collagen-induced arthritis (CIA) onset as determined by percent incidence in mice. Incidence=number of mice with at least one affected

paw/total number of mice per group. Figure 1A shows the effect of low dose range of ISIS 25302 anti-TNF-α antisense oligonucleotide in comparison to treatment by an anti-TNF-α mAb. Figure 1B shows the effect of high dose range treatment by ISIS 25302 in comparison to treatment by an 8 mismatch control oligonucleotide (ISIS 30782).

Figure 2 is a graph showing "total" histological scores for colon tissue from IL-$10^{-/-}$ mice treated with saline (vehicle), ISIS 25302 or 8MM Con. As recorded in Table 27. Results are expressed as mean " standard deviation (n=6). The asterisk indicates a significant difference ($p < 0.05$) in comparison to the vehicle group.

Figures 3A-B show the basal (Fig. 3A) and LPS-induced (Fig. 3B) levels of TNF-α secretion from colon tissue of IL-$10^{-/-}$ mice post-treatment with ISIS 25302 and the 8 base mismatch control oligonucleotide 30782 (8MM). Doses of oligonucleotide are shown in parentheses (mg/kg). Secretion levels (pg/gm-tissue) are shown in the y-axis. The mean values " standard deviation (n=7 to 9) are shown.

Figures 4A-B show the basal (Fig. 4A) and LPS-induced (Fig. 4B) levels of IFN-γ secretion from colon tissue of IL-$10^{-/-}$ mice post-treatment with ISIS 25302 and the 8 base mismatch control oligonucleotide 30782 (8MM). Doses of oligonucleotide are shown in parentheses (mg/kg). Secretion levels (pg/gm-tissue) are shown in the y-axis. The mean values " standard deviation (n=6 to 9) are shown.

Figures 5A-B show the efficacy of ISIS 25302 versus anti-mouse TNF-α mAb in the acute model of DSS-induced colitis. Fig. 5A shows the disease activity index (DAI). Fig. 5B shows the effect of different treatments on colon length. Results are expressed as the mean " S.E.M., where n=7. Asterisks show a significant difference from saline treated (*) or normal (*') group ($p<0.05$).

Figures 6A-B show that the prevention of acute colitis by ISIS 25302 in the DSS-induced colitis molecule is sequence-

dependent. Fig. 5A shows DAI versus treatment. Fig. 5B shows the effect of different treatments on colon length. Asterisks indicate significant differences from saline (*) or 1.0 mg/kg 8MM Con (*') treated group ($p<0.05$).

Figures 6A-B are graphs showing the efficacy of ISIS 25302 in the DSS-induced mouse model of chronic colitis based on DAI. Fig. 6A shows the mean DAI of each group over the course of the two cycle DSS-induced chronic colitis study. Fig. 6B shows the mean DAI at representative cycle times. The doses are indicated in parentheses (mg/kg). Results are expressed as the mean S.E.M., where n=8 to 10. Asterisks indicate statistical significance in comparison to the Vehicle group ($P<0.05$).

Figures 8A-B show histopathology of colon tissue from mice administered DSS in the two cycle chronic colitis model. Results are expressed as mean S.E.M. Fig. 8A shows the total inflammation and crypt scores. Acute inflammatory infiltrates consist of granulocytes, lymphocytes and plasma cells. Chronic inflammatory infiltrates consist of granulocytes, lymphocytes, plasma cells, monocytes and macrophages. Fig. 8B shows histological scores of different regions of the colon. PA=proximal acute inflammation score, DA=distal acute inflammation score, PC= proximal chronic inflammation score, DC=distal chronic inflammation score, PCS=proximal crypt score and DCS=distal crypt score. Asterisks indicate statistical significance in comparison to the Vehicle group ($p<0.05$).

Figure 9 shows TNF-α mRNA levels from longitudinal sections of colon tissue derived from each mouse at time of sacrifice in the chronic colitis model (mean S.E.M.). Group A=0.25 mg/kg ISIS 25302, group B=Vehicle, group C=anti-TNF mAb, group D=no treatment, group E=2.5 mg/kg ISIS 25302, group F=12.5 mg/kg ISIS 25302.

DETAILED DESCRIPTION OF THE INVENTION

TNF-α plays an important regulatory role in the immune response to various foreign agents. Overexpression of TNF-α results in a number of infectious and inflammatory diseases. As such, this cytokine represents an attractive target for treatment of such diseases. In particular, modulation of the expression of TNF-α may be useful for the treatment of diseases such as Crohn's disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, hepatitis, pancreatitis and asthma.

The present invention employs antisense compounds, particularly oligonucleotides, for use in modulating the function of nucleic acid molecules encoding TNF-α, ultimately modulating the amount of TNF-α produced. This is accomplished by providing oligonucleotides which specifically hybridize with nucleic acids, preferably mRNA, encoding TNF-α.

This relationship between an antisense compound such as an oligonucleotide and its complementary nucleic acid target, to which it hybridizes, is commonly referred to as "antisense". "Targeting" an oligonucleotide to a chosen nucleic acid target, in the context of this invention, is a multistep process. The process usually begins with identifying a nucleic acid sequence whose function is to be modulated. This may be, as examples, a cellular gene (or mRNA made from the gene) whose expression is associated with a particular disease state, or a foreign nucleic acid from an infectious agent. In the present invention, the targets are nucleic acids encoding TNF-α; in other words, a gene encoding TNF-α, or mRNA expressed from the TNF-α gene. mRNA which encodes TNF-α is presently the preferred target. The targeting process also includes determination of a site or sites within the nucleic acid sequence for the antisense interaction to occur such that modulation of gene expression will result.

In accordance with this invention, persons of ordinary skill in the art will understand that messenger RNA includes

not only the information to encode a protein using the three letter genetic code, but also associated ribonucleotides which form a region known to such persons as the 5'-untranslated region, the 3'-untranslated region, the 5' cap region and intron/exon junction ribonucleotides. Thus, oligonucleotides may be formulated in accordance with this invention which are targeted wholly or in part to these associated ribonucleotides as well as to the informational ribonucleotides. The oligonucleotide may therefore be specifically hybridizable with a transcription initiation site region, a translation initiation codon region, a 5' cap region, an intron/exon junction, coding sequences, a translation termination codon region or sequences in the 5'- or 3'-untranslated region. Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon." A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA molecule transcribed from a gene encoding TNF-α, regardless of the sequence(s) of such codons. It is also known in the art that a translation termination codon (or

"stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region," "AUG region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. This region is a preferred target region. Similarly, the terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon. This region is a preferred target region. The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Other preferred target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene. The 5' cap of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap. The 5' cap region may also be a preferred target region.

Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a pre-mRNA transcript to yield one or more mature mRNAs. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. mRNA splice sites, i.e., exon-exon or intron-exon junctions, may also be preferred target regions, and are particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular mRNA splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred targets. Targeting particular exons in alternatively spliced mRNAs may also be preferred. It has also been found that introns can also be effective, and therefore preferred, target regions for antisense compounds targeted, for example, to DNA or pre-mRNA.

Once the target site or sites have been identified, oligonucleotides are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired modulation.

"Hybridization", in the context of this invention, means hydrogen bonding, also known as Watson-Crick base pairing, between complementary bases, usually on opposite nucleic acid strands or two regions of a nucleic acid strand. Guanine and cytosine are examples of complementary bases which are known to form three hydrogen bonds between them. Adenine and thymine are examples of complementary bases which form two hydrogen bonds between them.

"Specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarily such that stable and specific binding occurs between the DNA or RNA target and the oligonucleotide.

It is understood that an oligonucleotide need not be 100% complementary to its target nucleic acid sequence to be

specifically hybridizable. An oligonucleotide is specifically hybridizable when binding of the oligonucleotide to the target interferes with the normal function of the target molecule to cause a loss of utility, and there is a sufficient degree of complementarily to avoid non-specific binding of the oligonucleotide to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment or, in the case of *in vitro* assays, under conditions in which the assays are conducted.

Hybridization of antisense oligonucleotides with mRNA interferes with one or more of the normal functions of mRNA. The functions of mRNA to be interfered with include all vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in by the RNA. Binding of specific protein(s) to the RNA may also be interfered with by antisense oligonucleotide hybridization to the RNA.

The overall effect of interference with mRNA function is modulation of expression of TNF-α. In the context of this invention "modulation" means either inhibition or stimulation; i.e., either a decrease or increase in expression. This modulation can be measured in ways which are routine in the art, for example by Northern blot assay of mRNA expression, or reverse transcriptase PER, as taught in the examples of the instant application or by Western blot or ELIZA assay of protein expression, or by an immunoprecipitation assay of protein expression. Effects of antisense oligonucleotides of the present invention on TNF-α expression can also be determined as taught in the examples of the instant application. Inhibition is presently a preferred form of modulation.

The oligonucleotides of this invention can be used in diagnostics, therapeutics, prophylaxis, and as research reagents and in kits. Since the oligonucleotides of this invention hybridize to nucleic acids encoding TNF-α, sandwich, colorimetric and other assays can easily be constructed to exploit this fact. Provision of means for detecting hybridization of oligonucleotides with the TNF-α gene or mRNA can routinely be accomplished. Such provision may include enzyme conjugation, radiolabelling or any other suitable detection systems. Kits for detecting the presence or absence of TNF-α may also be prepared.

The present invention is also suitable for diagnosing abnormal inflammatory states in tissue or other samples from patients suspected of having an inflammatory disease such as rheumatoid arthritis. The ability of the oligonucleotides of the present invention to inhibit inflammatory processes may be employed to diagnose such states. A number of assays may be formulated employing the present invention, which assays will commonly comprise contacting a tissue sample with an oligonucleotide of the invention under conditions selected to permit detection and, usually, quantitation of such inhibition. In the context of this invention, to "contact" tissues or cells with an oligonucleotide or oligonucleotides means to add the oligonucleotide(s), usually in a liquid carrier, to a cell suspension or tissue sample, either *in vitro* or *ex vivo*, or to administer the oligonucleotide(s) to cells or tissues within an animal.

The oligonucleotides of this invention may also be used for research purposes. Thus, the specific hybridization exhibited by the oligonucleotides may be used for assays, purifications, cellular product preparations and in other methodologies which may be appreciated by persons of ordinary skill in the art.

In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of

ribonucleic acid or deoxyribonucleic acid. This term includes oligonucleotides composed of naturally-occurring nucleobases, sugars and covalent intersugar (backbone) linkages as well as oligonucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced binding to target and increased stability in the presence of nucleases.

The antisense compounds in accordance with this invention preferably comprise from about 5 to about 50 nucleobases. Particularly preferred are antisense oligonucleotides comprising from about 8 to about 30 nucleobases (i.e., from about 8 to about 30 linked nucleosides). As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidine. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn the respective ends of this linear polymeric structure can be further joined to form a circular structure, however, open linear structures are generally preferred. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing

modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Preferred modified oligonucleotide backbones include, for example, phosphorothioates, choral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and choral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to U.S. Patent 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These

include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Patent 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439.

In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S.: 5,539,082; 5,714,331; and 5,719,262. Further teaching of PNA compounds can be found in Nielsen *et al.* (*Science*, **1991**, *254*, 1497-1500).

Most preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular $-CH_2-NH-O-CH_2-$, $-CH_2-N(CH_3)-O-CH_2$ [known as a methylene (methylimino) or MMI backbone], $-CH_2-O-N(CH_3)-CH_2-$, $-CH_2-N(CH_3)-N(CH_3)-CH_2-$ and $-O-N(CH_3)-CH_2-CH_2$ [wherein the native phosphodiester backbone is represented as $-O-P-O-CH_2-$] of the above referenced U.S. Patent 5,489,677, and the amide backbones of the above referenced U.S. Patent 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. Patent 5,034,506.

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl, O-alkyl-O-alkyl, O-, S-, or N-alkenyl, or O-, S- or N-alkynyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_2ON(CH_3)_2$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta* **1995**, *78*, 486-504) i.e., an alkoxyalkoxy group.

Other preferred modifications include 2'-methoxy (2'-O-CH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugars structures include, but are not limited to, U.S. Patent 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920.

Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C or m5c), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Patent

3,687,808, those disclosed in the *Concise Encyclopedia Of Polymer Science And Engineering* **1990**, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, those disclosed by Englisch et al. *(Angewandte Chemie, International Edition* **1991**, *30*, 613-722), and those disclosed by Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds., *Antisense Research and Applications* **1993**, CRC Press, Boca Raton, pages 289-302. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidine, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-Methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds., *Antisense Research and Applications* **1993**, CRC Press, Boca Raton, pages 276-278) and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative United States patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Patent 3,687,808, as well as U.S. Patent 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; and 5,681,941.

Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA **1989**, *86*, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Lett. **1994**, *4*,

1053-1059), a thioether, e.g., hexyl-*S*-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci. **1992**, *660*, 306-309; Manoharan et al., Bioorg. Med. Chem. Let. **1993**, *3*, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res. **1992**, *20*, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J. **1991**, *10*, 1111-1118; Kabanov et al., FEBS Lett. **1990**, *259*, 327-330; Svinarchuk et al., Biochimie **1993**, *75*, 49-54), a phospholipid, e.g., di-hexadecyl-*rac*-glycerol or triethylammonium 1,2-di-O-hexadecyl-*rac*-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett. **1995**, *36*, 3651-3654; Shea et al., Nucl. Acids Res. **1990**, *18*, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides **1995**, *14*, 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett. **1995**, *36*, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta **1995**, *1264*, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther. **1996**, *277*, 923-937).

Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S. Patent 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941.

The present invention also includes oligonucleotides which are chimeric oligonucleotides. "Chimeric" oligonucleotides or "chimeras," in the context of this invention, are oligonucleotides which contain two or more chemically distinct regions, each made up of at least one nucleotide. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of antisense inhibition of gene expression. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art. This RNAse H-mediated cleavage of the RNA target is distinct from the use of ribozymes to cleave nucleic acids. Ribozymes are not comprehended by the present invention.

Examples of chimeric oligonucleotides include but are not limited to "gapmers," in which three distinct regions are present, normally with a central region flanked by two regions which are chemically equivalent to each other but distinct from the gap. A preferred example of a gapmer is an oligonucleotide in which a central portion (the "gap") of the oligonucleotide serves as a substrate for RNase H and is preferably composed of 2'-deoxynucleotides, while the flanking portions (the 5' and 3' "wings") are modified to have greater affinity for the target RNA molecule but are unable to support nuclease activity (e.g., fluoro- or 2'-O-methoxyethyl-substituted). Chimeric oligonucleotides are not limited to

those with modifications on the sugar, but may also include oligonucleosides or oligonucleotides with modified backbones, e.g., with regions of phosphorothioate (P=S) and phosphodiester (P=O) backbone linkages or with regions of MMI and P=S backbone linkages. Other chimeras include "wingmers," also known in the art as "hemimers," that is, oligonucleotides with two distinct regions. In a preferred example of a wingmer, the 5' portion of the oligonucleotide serves as a substrate for RNase H and is preferably composed of 2'-deoxynucleotides, whereas the 3' portion is modified in such a fashion so as to have greater affinity for the target RNA molecule but is unable to support nuclease activity (e.g., 2'-fluoro- or 2'-O-methoxyethyl- substituted), or vice-versa. In one embodiment, the oligonucleotides of the present invention contain a 2'-O-methoxyethyl ($2'\text{-}O\text{-}CH_2CH_2OCH_3$) modification on the sugar moiety of at least one nucleotide. This modification has been shown to increase both affinity of the oligonucleotide for its target and nuclease resistance of the oligonucleotide. According to the invention, one, a plurality, or all of the nucleotide subunits of the oligonucleotides of the invention may bear a 2'-O-methoxyethyl ($-O\text{-}CH_2CH_2OCH_3$) modification. Oligonucleotides comprising a plurality of nucleotide subunits having a 2'-O-methoxyethyl modification can have such a modification on any of the nucleotide subunits within the oligonucleotide, and may be chimeric oligonucleotides. Aside from or in addition to 2'-O-methoxyethyl modifications, oligonucleotides containing other modifications which enhance antisense efficacy, potency or target affinity are also preferred. Chimeric oligonucleotides comprising one or more such modifications are presently preferred.

The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including Applied

Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the talents of the routineer. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and 2'-alkoxy or 2'-alkoxyalkoxy derivatives, including 2'-O-methoxyethyl oligonucleotides (Martin, P., *Helv. Chim. Acta* **1995**, *78*, 486-504). It is also well known to use similar techniques and commercially available modified amidites and controlled-pore glass (CPG) products such as biotin, fluorescein, acridine or psoralen-modified amidites and/or CPG (available from Glen Research, Sterling, VA) to synthesize fluorescently labeled, biotinylated or other conjugated oligonucleotides.

The antisense compounds of the present invention include bioequivalent compounds, including pharmaceutically acceptable salts and prodrugs. This is intended to encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of the nucleic acids of the invention and prodrugs of such nucleic acids. APharmaceutically acceptable salts@ are physiologically and pharmaceutically acceptable salts of the nucleic acids of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto (see, for example, Berge et al., "Pharmaceutical Salts," *J. of Pharma Sci.* **1977**, *66*, 1-19).

For oligonucleotides, examples of pharmaceutically acceptable salts include but are not limited to (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as spermine and spermidine, etc.; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, hydrobromic

acid, sulfuric acid, phosphoric acid, nitric acid and the like; 8 salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, naphthalenedisulfonic acid, polygalacturonic acid, and the like; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine.

The oligonucleotides of the invention may additionally or alternatively be prepared to be delivered in a Aprodrug@ form. The term Aprodrug@ indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate] derivatives according to the methods disclosed in WO 93/24510.

For therapeutic or prophylactic treatment, oligonucleotides are administered in accordance with this invention. Oligonucleotide compounds of the invention may be formulated in a pharmaceutical composition, which may include pharmaceutically acceptable carriers, thickeners, diluents, buffers, preservatives, surface active agents, neutral or cationic lipids, lipid complexes, liposomes, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients and the like in addition to the oligonucleotide. Such compositions and formulations are comprehended by the present invention.

Pharmaceutical compositions comprising the oligonucleotides of the present invention may include penetration enhancers in order to enhance the alimentary delivery of the oligonucleotides. Penetration enhancers may

be classified as belonging to one of five broad categories, i.e., fatty acids, bile salts, chelating agents, surfactants and non-surfactants (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems* **1991**, *8,* 91-192; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems* **1990**, *7,* 1-33). One or more penetration enhancers from one or more of these broad categories may be included. Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, recinleate, monoolein (a.k.a. 1-monooleoyl-*rac*-glycerol), dilaurin, caprylic acid, arachidonic acid, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, mono- and di-glycerides and physiologically acceptable salts thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems* **1991**, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems* **1990**, *7,* 1; El-Hariri et al., *J. Pharm. Pharmacol.* **1992** *44,* 651-654).

The physiological roles of bile include the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (Brunton, Chapter 38 *In: Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al., eds., McGraw-Hill, New York, NY, **1996**, pages 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus, the term "bile salt" includes any of the naturally occurring components of bile as well as any of their synthetic derivatives.

Complex formulations comprising one or more penetration enhancers may be used. For example, bile salts may be used in combination with fatty acids to make complex formulations.

Chelating agents include, but are not limited to, disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and

homovanilate), *N*-acyl derivatives of collagen, laureth-9 and *N*-amino acyl derivatives of beta-diketones (enamines)(Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems* **1991**, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems* **1990**, *7*, 1-33; Buur et al., *J. Control Rel.* **1990**, *14*, 43-51). Chelating agents have the added advantage of also serving as DNase inhibitors.

Surfactants include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems* **1991**, page 92); and perfluorochemical emulsions, such as FC-43 (Takahashi et al., *J. Pharm. Pharmacol.* **1988**, *40*, 252-257).

Non-surfactants include, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems* **1991**, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin and phenylbutazone (Yamashita et al., *J. Pharm. Pharmacol.* **1987**, *39*, 621-626).

As used herein, "carrier compound" refers to a nucleic acid, or analog thereof, which is inert (*i.e.*, does not possess biological activity *per se*) but is recognized as a nucleic acid by *in vivo* processes that reduce the bioavailability of a nucleic acid having biological activity by, for example, degrading the biologically active nucleic acid or promoting its removal from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to competition between the carrier compound and the nucleic acid for a common receptor. In contrast to a carrier compound, a "pharmaceutically acceptable

carrier" (excipient) is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The pharmaceutically acceptable carrier may be liquid or solid and is selected with the planned manner of administration in mind so as to provide for the desired bulk, consistency, *etc.*, when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutically acceptable carriers include, but are not limited to, binding agents (e.g., pregelatinized maize starch, polyvinyl-pyrrolidone or hydroxypropyl methylcellulose, *etc.*); fillers (e.g., lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, *etc.*); lubricants (e.g., magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, etc.); disintegrates (e.g., starch, sodium starch glycolate, etc.); or wetting agents (e.g., sodium lauryl sulphate, etc.). Sustained release oral delivery systems and/or enteric coatings for orally administered dosage forms are described in U.S. Patents 4,704,295; 4,556,552; 4,309,406; and 4,309,404.

The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions may contain additional compatible pharmaceutically-active materials such as, e.g., antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added,

should not unduly interfere with the biological activities of the components of the compositions of the invention.

Regardless of the method by which the oligonucleotides of the invention are introduced into a patient, colloidal dispersion systems may be used as delivery vehicles to enhance the *in vivo* stability of the oligonucleotides and/or to target the oligonucleotides to a particular organ, tissue or cell type. Colloidal dispersion systems include, but are not limited to, macromolecule complexes, nanocapsules, microspheres, beads and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, liposomes and lipid:oligonucleotide complexes of uncharacterized structure. A preferred colloidal dispersion system is a plurality of liposomes. Liposomes are microscopic spheres having an aqueous core surrounded by one or more outer layers made up of lipids arranged in a bilayer configuration (see, generally, Chonn et al., *Current Op. Biotech.* **1995**, *6,* 698-708).

The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic, vaginal, rectal, intranasal, epidermal, and transdermal), oral or parenteral. Parenteral administration includes intravenous drip, subcutaneous, intraperitoneal or intramuscular injection, pulmonary administration, e.g., by inhalation or insufflation, or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration.

Formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

Compositions for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable.

Compositions for parenteral administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives. In some cases it may be more effective to treat a patient with an oligonucleotide of the invention in conjunction with other traditional therapeutic modalities in order to increase the efficacy of a treatment regimen. In the context of the invention, the term "treatment regimen" is meant to encompass therapeutic, palliative and prophylactic modalities. For example, a patient may be treated with conventional chemotherapeutic agents such as those used for tumor and cancer treatment. When used with the compounds of the invention, such chemotherapeutic agents may be used individually, sequentially, or in combination with one or more other such chemotherapeutic agents.

The formulation of therapeutic compositions and their subsequent administration is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC_{50}s found to be effective *in vitro* and in *in vivo* animal models. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more

daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

Thus, in the context of this invention, by "therapeutically effective amount" is meant the amount of the compound which is required to have a therapeutic effect on the treated individual. This amount, which will be apparent to the skilled artisan, will depend upon the age and weight of the individual, the type of disease to be treated, perhaps even the gender of the individual, and other factors which are routinely taken into consideration when designing a drug treatment. A therapeutic effect is assessed in the individual by measuring the effect of the compound on the disease state in the animal.

The following examples illustrate the present invention and are not intended to limit the same.

EXAMPLES

EXAMPLE 1: Synthesis of Oligonucleotides

Unmodified oligodeoxynucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 380B) using standard phosphoramidite chemistry with oxidation by iodine. β- cyanoethyldiisopropyl-phosphoramidites are purchased from Applied Biosystems (Foster City, CA). For phosphorothioate oligonucleotides, the standard oxidation bottle was replaced by a 0.2 M solution of ^{3}H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the stepwise thiation of the phosphite linkages. The thiation

cycle wait step was increased to 68 seconds and was followed by the capping step. Cytosines may be 5-methyl cytosines. (5-methyl deoxycytidine phosphoramidites available from Glen Research, Sterling, VA or Amersham Pharmacia Biotech, Piscataway, NJ)

2'-methoxy oligonucleotides are synthesized using 2'-methoxy β-cyanoethyldiisopropyl-phosphoramidites (Chemgenes, Needham, MA) and the standard cycle for unmodified oligonucleotides, except the wait step after pulse delivery of tetrazole and base is increased to 360 seconds. Other 2'-alkoxy oligonucleotides are synthesized by a modification of this method, using appropriate 2'-modified amidites such as those available from Glen Research, Inc., Sterling, VA.

2'-fluoro oligonucleotides are synthesized as described in Kawasaki et al. (*J. Med. Chem.* **1993**, *36*, 831-841). Briefly, the protected nucleoside N^6-benzoyl-2'-deoxy-2'-fluoroadenosine is synthesized utilizing commercially available 9-β-D-arabinofuranosyladenine as starting material and by modifying literature procedures whereby the 2'-α-fluoro atom is introduced by a S_N2-displacement of a 2'-β-O-trifyl group. Thus N^6-benzoyl-9-β-D-arabinofuranosyladenine is selectively protected in moderate yield as the 3',5'-ditetrahydropyranyl (THP) intermediate. Deprotection of the THP and N^6-benzoyl groups is accomplished using standard methodologies. Standard methods are also used to obtain the 5'-dimethoxytrityl- (DMT) and 5'-DMT-3'-phosphoramidite intermediates.

The synthesis of 2'-deoxy-2'-fluoroguanosine is accomplished using tetraisopropyldisiloxanyl (TPDS) protected 9-β-D-arabinofuranosylguanine as starting material, and conversion to the intermediate diisobutyryl-arabinofuranosylguanosine. Deprotection of the TPDS group is followed by protection of the hydroxyl group with THP to give diisobutyryl di-THP protected arabinofuranosylguanine. Selective O-deacylation and triflation is followed by

treatment of the crude product with fluoride, then deprotection of the THP groups. Standard methodologies are used to obtain the 5'-DMT- and 5'-DMT-3'-phosphoramidites.

Synthesis of 2'-deoxy-2'-fluorouridine is accomplished by the modification of a known procedure in which 2, 2'-anhydro-1-β-D-arabinofuranosyluracil is treated with 70% hydrogen fluoride-pyridine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-deoxy-2'-fluorocytidine is synthesized via amination of 2'-deoxy-2'-fluorouridine, followed by selective protection to give N^4-benzoyl-2'-deoxy-2'-fluorocytidine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-(2-methoxyethyl)-modified amidites were synthesized according to Martin, P. (*Helv. Chim. Acta* **1995**, *78*, 486-506). For ease of synthesis, the last nucleotide may be a deoxynucleotide. 2'-O-$CH_2CH_2OCH_3$-cytosines may be 5-methyl cytosines.

Synthesis of 5-Methyl cytosine monomers:

2,2'-Anhydro[1-(β-D-arabinofuranosyl)-5-methyluridine]:

5-Methyluridine (ribosylthymine, commercially available through Yamasa, Choshi, Japan) (72.0 g, 0.279 M), diphenylcarbonate (90.0 g, 0.420 M) and sodium bicarbonate (2.0 g, 0.024 M) were added to DMF (300 mL). The mixture was heated to reflux, with stirring, allowing the evolved carbon dioxide gas to be released in a controlled manner. After 1 hour, the slightly darkened solution was concentrated under reduced pressure. The resulting syrup was poured into diethylether (2.5 L), with stirring. The product formed a gum. The ether was decanted and the residue was dissolved in a minimum amount of methanol (ca. 400 mL). The solution was poured into fresh ether (2.5 L) to yield a stiff gum. The ether was decanted and the gum was dried in a vacuum oven (60EC at 1 mm Hg for 24 hours) to give a solid which was crushed to a light tan

powder (57 g, 85% crude yield). The material was used as is for further reactions.

2'-O-Methoxyethyl-5-methyluridine:

2,2'-Anhydro-5-methyluridine (195 g, 0.81 M), tris(2-methoxyethyl)borate (231 g, 0.98 M) and 2-methoxyethanol (1.2 L) were added to a 2 L stainless steel pressure vessel and placed in a pre-heated oil bath at 160EC. After heating for 48 hours at 155-160EC, the vessel was opened and the solution evaporated to dryness and triturated with MeOH (200 mL). The residue was suspended in hot acetone (1 L). The insoluble salts were filtered, washed with acetone (150 mL) and the filtrate evaporated. The residue (280 g) was dissolved in CH_3CN (600 mL) and evaporated. A silica gel column (3 kg) was packed in CH_2Cl_2/acetone/MeOH (20:5:3) containing 0.5% Et_3NH. The residue was dissolved in CH_2Cl_2 (250 mL) and adsorbed onto silica (150 g) prior to loading onto the column. The product was eluted with the packing solvent to give 160 g (63%) of product.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine:

2'-O-Methoxyethyl-5-methyluridine (160 g, 0.506 M) was co-evaporated with pyridine (250 mL) and the dried residue dissolved in pyridine (1.3 L). A first aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the mixture stirred at room temperature for one hour. A second aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the reaction stirred for an additional one hour. Methanol (170 mL) was then added to stop the reaction. HPLC showed the presence of approximately 70% product. The solvent was evaporated and triturated with CH_3CN (200 mL). The residue was dissolved in $CHCl_3$ (1.5 L) and extracted with 2x500 mL of saturated $NaHCO_3$ and 2x500 mL of saturated NaCl. The organic phase was dried over Na_2SO_4, filtered and evaporated. 275 g of residue was obtained. The residue was purified on a 3.5

kg silica gel column, packed and eluted with EtOAc/-Hexane/Acetone (5:5:1) containing 0.5% Et_3NH. The pure fractions were evaporated to give 164 g of product. Approximately 20 g additional was obtained from the impure fractions to give a total yield of 183 g (57%).

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-uridine:

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (106 g, 0.167 M), DMF/pyridine (750 mL of a 3:1 mixture prepared from 562 mL of DMF and 188 mL of pyridine) and acetic anhydride (24.38 mL, 0.258 M) were combined and stirred at room temperature for 24 hours. The reaction was monitored by tlc by first quenching the tlc sample with the addition of MeOH. Upon completion of the reaction, as judged by tlc, MeOH (50 mL) was added and the mixture evaporated at 35EC. The residue was dissolved in $CHCl_3$ (800 mL) and extracted with 2x200 mL of saturated sodium bicarbonate and 2x200 mL of saturated NaCl. The water layers were back extracted with 200 mL of $CHCl_3$. The combined organics were dried with sodium sulfate and evaporated to give 122 g of residue (approx. 90% product). The residue was purified on a 3.5 kg silica gel column and eluted using EtOAc/Hexane(4:1). Pure product fractions were evaporated to yield 96 g (84%).

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine:

A first solution was prepared by dissolving 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (96 g, 0.144 M) in CH_3CN (700 mL) and set aside. Triethylamine (189 mL, 1.44 M) was added to a solution of triazole (90 g, 1.3 M) in CH_3CN (1 L), cooled to -5EC and stirred for 0.5 hours using an overhead stirrer. $POCl_3$ was added dropwise, over a 30 minute period, to the stirred solution maintained at 0-10EC, and the resulting mixture stirred for an additional 2 hours.

The first solution was added dropwise, over a 45 minute period, to the later solution. The resulting reaction mixture was stored overnight in a cold room. Salts were filtered from the reaction mixture and the solution was evaporated. The residue was dissolved in EtOAc (1 L) and the insoluble solids were removed by filtration. The filtrate was washed with 1x300 mL of $NaHCO_3$ and 2x300 mL of saturated NaCl, dried over sodium sulfate and evaporated. The residue was triturated with EtOAc to give the title compound.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine:

A solution of 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine (103 g, 0.141 M) in dioxane (500 mL) and NH_4OH (30 mL) was stirred at room temperature for 2 hours. The dioxane solution was evaporated and the residue azeotroped with MeOH (2x200 mL). The residue was dissolved in MeOH (300 mL) and transferred to a 2 liter stainless steel pressure vessel. MeOH (400 mL) saturated with NH_3 gas was added and the vessel heated to 100EC for 2 hours (tlc showed complete conversion). The vessel contents were evaporated to dryness and the residue was dissolved in EtOAc (500 mL) and washed once with saturated NaCl (200 mL). The organics were dried over sodium sulfate and the solvent was evaporated to give 85 g (95%) of the title compound.

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-cytidine:

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (85 g, 0.134 M) was dissolved in DMF (800 mL) and benzoic anhydride (37.2 g, 0.165 M) was added with stirring. After stirring for 3 hours, tlc showed the reaction to be approximately 95% complete. The solvent was evaporated and the residue azeotroped with MeOH (200 mL). The residue was dissolved in $CHCl_3$ (700 mL) and extracted with saturated $NaHCO_3$ (2x300 mL) and saturated NaCl (2x300 mL), dried over $MgSO_4$ and

evaporated to give a residue (96 g). The residue was chromatographed on a 1.5 kg silica column using EtOAc/Hexane (1:1) containing 0.5% Et_3NH as the eluting solvent. The pure product fractions were evaporated to give 90 g (90%) of the title compound.

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine-3'-amidite:

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (74 g, 0.10 M) was dissolved in CH_2Cl_2 (1 L). Tetrazole diisopropylamine (7.1 g) and 2-cyanoethoxy-tetra-(isopropyl)phosphite (40.5 mL, 0.123 M) were added with stirring, under a nitrogen atmosphere. The resulting mixture was stirred for 20 hours at room temperature (tlc showed the reaction to be 95% complete). The reaction mixture was extracted with saturated $NaHCO_3$ (1x300 mL) and saturated NaCl (3x300 mL). The aqueous washes were back-extracted with CH_2Cl_2 (300 mL), and the extracts were combined, dried over $MgSO_4$ and concentrated. The residue obtained was chromatographed on a 1.5 kg silica column using EtOAc\Hexane (3:1) as the eluting solvent. The pure fractions were combined to give 90.6 g (87%) of the title compound.

5-methyl-2'-deoxycytidine (5-me-C) containing oligonucleotides were synthesized according to published methods (Sanghvi et al., *Nucl. Acids Res.* **1993**, *21*, 3197-3203) using commercially available phosphoramidites (Glen Research, Sterling VA or ChemGenes, Needham MA).

Oligonucleotides having methylene(methylimino) (MMI) backbones were synthesized according to U.S. Patent 5,378,825, which is coassigned to the assignee of the present invention and is incorporated herein in its entirety. For ease of synthesis, various nucleoside dimers containing MMI linkages were synthesized and incorporated into oligonucleotides. Other nitrogen-containing backbones are synthesized according to WO

92/20823 which is also coassigned to the assignee of the present invention and incorporated herein in its entirety.

Oligonucleotides having amide backbones are synthesized according to De Mesmaeker et al. (*Acc. Chem. Res.* **1995**, *28*, 366-374). The amide moiety is readily accessible by simple and well-known synthetic methods and is compatible with the conditions required for solid phase synthesis of oligonucleotides.

Oligonucleotides with morpholino backbones are synthesized according to U.S. Patent 5,034,506 (Summerton and Weller).

Peptide-nucleic acid (PNA) oligomers are synthesized according to P.E. Nielsen et al. (*Science* **1991**, *254*, 1497-1500). After cleavage from the controlled pore glass column (Applied Biosystems) and deblocking in concentrated ammonium hydroxide at 55EC for 18 hours, the oligonucleotides are purified by precipitation twice out of 0.5 M NaCl with 2.5 volumes ethanol. Synthesized oligonucleotides were analyzed by polyacrylamide gel electrophoresis on denaturing gels and judged to be at least 85% full length material. The relative amounts of phosphorothioate and phosphodiester linkages obtained in synthesis were periodically checked by ^{31}P nuclear magnetic resonance spectroscopy, and for some studies oligonucleotides were purified by HPLC, as described by Chiang et al. (*J. Biol. Chem.* **1991**, *266*, 18162). Results obtained with HPLC-purified material were similar to those obtained with non-HPLC purified material.

EXAMPLE 2: Human TNF-α Oligodeoxynucleotide Sequences

Antisense oligonucleotides were designed to target human TNF-α. Target sequence data are from the TNF-α cDNA sequence published by Nedwin,G.E. et al. (*Nucleic Acids Res.* **1985**, *13*, 6361-6373); Genbank accession number X02910, provided herein as SEQ ID NO: 1. Oligodeoxynucleotides were synthesized primarily with phosphorothioate linkages. Oligonucleotide

sequences are shown in Table 1. Oligonucleotide 14640 (SEQ ID NO. 2) is a published TNF-α antisense oligodeoxynucleotide targeted to the start site of the TNF-α gene (Hartmann,G., et al., *Antisense Nucleic Acid Drug Dev.*, **1996**, *6*, 291-299). Oligonucleotide 2302 (SEQ ID NO. 41) is an antisense oligodeoxynucleotide targeted to the human intracellular adhesion molecule-1 (ICAM-1) and was used as an unrelated (negative) target control. Oligonucleotide 13664 (SEQ ID NO. 42) is an antisense oligodeoxynucleotide targeted to the Herpes Simplex Virus type 1 and was used as an unrelated target control.

NeoHK cells, human neonatal foreskin keratinocytes (obtained from Cascade Biologicals, Inc., Portland, OR) were cultured in Keratinocyte medium containing the supplied growth factors (Life Technologies, Rockville, MD).

At assay time, the cells were between 70% and 90% confluent. The cells were incubated in the presence of Keratinocyte medium, without the supplied growth factors added, and the oligonucleotide formulated in LIPOFECTIN7 (Life Technologies), a 1:1 (w/w) liposome formulation of the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-n,n,n-trimethylammonium chloride (DOTMA), and dioleoyl phosphotidylethanolamine (DOPE) in membrane filtered water. For an initial screen, the oligonucleotide concentration was 300 nM in 9 μg/mL LIPOFECTIN7. Treatment was for four hours. After treatment, the medium was removed and the cells were further incubated in Keratinocyte medium containing the supplied growth factors and 100 nM phorbol 12-myristate 13-acetate (PMA, Sigma, St. Louis, MO). mRNA was analyzed 2 hours post-induction with PMA. Protein levels were analyzed 12 to 20 hours post-induction.

Total mRNA was isolated using the RNEASY7 Mini Kit (Qiagen, Valencia, CA; similar kits from other manufacturers may also be used), separated on a 1% agarose gel, transferred to HYBOND™-N+ membrane (Amersham Pharmacia Biotech,

Piscataway, NJ), a positively charged nylon membrane, and probed. A TNF-α probe consisted of the 505 bp EcoRI-HindIII fragment from BBG 18 (R&D Systems, Minneapolis, MN), a plasmid containing human TNF-α cDNA. A glyceraldehyde 3-phosphate dehydrogenase (G3PDH) probe consisted of the 1.06 kb HindIII fragment from pHcGAP (American Type Culture Collection, Manassas, VA), a plasmid containing human G3PDH cDNA. The restriction fragments were purified from low-melting temperature agarose, as described in Maniatis, T., et al., *Molecular Cloning: A Laboratory Manual*, **1989** and labeled with REDIVUE™ ^{32}P-dCTP (Amersham Pharmacia Biotech, Piscataway, NJ) and PRIME-A-GENE7 labeling kit (Promega, Madison, WI). mRNA was quantitated by a PhosphoImager (Molecular Dynamics, Sunnyvale, CA). Secreted TNF-α protein levels were measured using a human TNF-α ELIZA kit (R&D Systems, Minneapolis, MN or Genzyme, Cambridge, MA).

TABLE 1

Nucleotide Sequences of Human TNF-α Phosphorothioate Oligodeoxynucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
14640	CATGCTTTCAGTGCTCAT	2	0796-0813	AUG
14641	TGAGGGAGCGTCTGCTGGCT	3	0615-0634	5'-UTR
14642	GTGCTCATGGTGTCCTTTCC	4	0784-0803	AUG
14643	TAATCACAAGTGCAAACATA	5	3038-3057	3'-UTR
14644	TACCCCGGTCTCCCAAATAA	6	3101-3120	3'-UTR
14810	GTGCTCATGGTGTCCTTTCC	4	0784-0803	AUG
14811	AGCACCGCCTGGAGCCCT	7	0869-0886	coding
14812	GCTGAGGAACAAGCACCGCC	8	0878-0897	coding
14813	AGGCAGAAGAGCGTGGTGGC	9	0925-0944	coding
14814	AAAGTGCAGCAGGCAGAAGA	10	0935-0954	coding
14815	TTAGAGAGAGGTCCCTGG	11	1593-1610	coding

14816	TGACTGCCTGGGCCAGAG	12	1617-1634	junction
14817	GGGTTCGAGAAGATGATC	13	1822-1839	junction
14818	GGGCTACAGGCTTGTCACTC	14	1841-1860	coding
14820	CCCCTCAGCTTGAGGGTTTG	15	2171-2190	junction
14821	CCATTGGCCAGGAGGGCATT	16	2218-2237	coding
14822	ACCACCAGCTGGTTATCTCT	17	2248-2267	coding
14823	CTGGGAGTAGATGAGGTACA	18	2282-2301	coding
14824	CCCTTGAAGAGGACCTGGGA	19	2296-2315	coding
14825	GGTGTGGGTGAGGAGCACAT	20	2336-2355	coding
14826	GTCTGGTAGGAGACGGCGAT	21	2365-2384	coding
14827	GCAGAGAGGAGGTTGACCTT	22	2386-2405	coding
14828	GCTTGGCCTCAGCCCCCTCT	23	2436-2455	coding
14829	CCTCCCAGATAGATGGGCTC	24	2464-2483	coding
14830	CCCTTCTCCAGCTGGAAGAC	25	2485-2504	coding
14831	ATCTCAGCGCTGAGTCGGTC	26	2506-2525	coding
14832	TCGAGATAGTCGGGCCGATT	27	2527-2546	coding
14833	AAGTAGACCTGCCCAGACTC	28	2554-2573	coding
14834	GGATGTTCGTCCTCCTCACA	29	2588-2607	STOP
14835	ACCCTAAGCCCCCAATTCTC	30	2689-2708	3'-UTR
14836	CCACACATTCCTGAATCCCA	31	2758-2777	3'-UTR
14837	AGGCCCCAGTGAGTTCTGGA	32	2825-2844	3'-UTR
14838	GTCTCCAGATTCCAGATGTC	33	2860-2879	3'-UTR
14839	CTCAAGTCCTGCAGCATTCT	34	2902-2921	3'-UTR
14840	TGGGTCCCCCAGGATACCCC	35	3115-3134	3'-UTR
14841	ACGGAAAACATGTCTGAGCC	36	3151-3170	3'-UTR
14842	CTCCGTTTTCACGGAAAACA	37	3161-3180	3'-UTR
14843	GCCTATTGTTCAGCTCCGTT	38	3174-3193	3'-UTR
14844	GGTCACCAAATCAGCATTGT	39	3272-3292	3'-UTR
14845	GAGGCTCAGCAATGAGTGAC	40	3297-3316	3'-UTR
2302	GCCCAAGCTGGCATCCGTCA	41	target control	
13664	GCCGAGGTCCATGTCGTACGC	42	target control	

[1] "C" residues are 5-methyl-cytosines except "C" residues are unmodified cytidines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

Results are shown in Table 2. Oligonucleotides 14828 (SEQ ID NO. 23), 14829 (SEQ ID NO. 24), 14832 (SEQ ID NO. 27), 14833 (SEQ ID NO. 28), 14834 (SEQ ID NO. 29), 14835 (SEQ ID NO. 30), 14836 (SEQ ID NO. 31), 14839 (SEQ ID NO. 34), 14840 (SEQ ID NO. 35), and 14844 (SEQ ID NO. 39) inhibited TNF-α expression by approximately 50% or more. Oligonucleotides 14828 (SEQ ID NO. 23), 14834 (SEQ ID NO. 29), and 14840 (SEQ ID NO. 35) gave better than 70% inhibition.

TABLE 2

Inhibition of Human TNF-α mRNA Expression by Phosphorothioate Oligodeoxynucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
basal	---	---	16%	---
induced	---	---	100%	0%
13664	42	control	140%	---
14640	2	AUG	61%	39%
14641	3	5'-UTR	95%	5%
14642	4	AUG	131%	---
14810	4	AUG	111%	---
14815	11	coding	85%	15%
14816	12	junction	106%	---
14817	13	junction	97%	3%
14818	14	coding	64%	36%
14820	15	junction	111%	---
14821	16	coding	91%	9%
14822	17	coding	57%	43%

14827	22	coding	67%	33%
14828	23	coding	27%	73%
14829	24	coding	33%	67%
14830	25	coding	71%	29%
14831	26	coding	62%	38%
14832	27	coding	40%	60%
14833	28	coding	43%	57%
14834	29	STOP	26%	74%
14835	30	3'-UTR	32%	68%
14836	31	3'-UTR	40%	60%
14837	32	3'-UTR	106%	---
14838	33	3'-UTR	70%	30%
14839	34	5'-UTR	49%	51%
14840	35	3'-UTR	28%	72%
14841	36	3'-UTR	60%	40%
14842	37	3'-UTR	164%	---
14843	38	3'-UTR	67%	33%
14844	39	3'-UTR	46%	54%
14845	40	3'-UTR	65%	35%

EXAMPLE 3: Dose response of antisense phosphorothioate oligodeoxynucleotide effects on human TNF-α mRNA levels in NeoHK cells

Four of the more active oligonucleotides from the initial screen were chosen for dose response assays. These include oligonucleotides 14828 (SEQ ID NO. 23), 14833 (SEQ ID NO. 28), 14834 (SEQ ID NO. 29) and 14839 (SEQ ID NO. 34). NeoHK cells were grown, treated and processed as described in Example 2. LIPOFECTIN7 was added at a ratio of 3 µg/mL per 100 nM of oligonucleotide. The control included LIPOFECTIN7 at a concentration of 9 µg/mL. The effect of the TNF-α antisense oligonucleotides was normalized to the non-specific target control. Results are shown in Table 3. Each

oligonucleotide showed a dose response effect with maximal inhibition greater than 70%. Oligonucleotides 14828 (SEQ ID NO. 23) had an IC_{50} of approximately 185 nM. Oligonucleotides 14833 (SEQ ID NO. 28) had an IC_{50} of approximately 150 nM. Oligonucleotides 14834 (SEQ ID NO. 29) and 14839 (SEQ ID NO. 34) had an IC_{50} of approximately 140 nM.

TABLE 3

Dose Response of NeoHK Cells to TNF-α Antisense Phosphorothioate Oligodeoxynucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
2302	41	control	25 nM	100%	---
"	"	"	50 nM	100%	---
"	"	"	100 nM	100%	---
"	"	"	200 nM	100%	---
"	"	"	300 nM	100%	---
14828	23	coding	25 nM	122%	---
"	"	"	50 nM	97%	3%
"	"	"	100 nM	96%	4%
"	"	"	200 nM	40%	60%
"	"	"	300 nM	22%	78%
14833	28	coding	25 nM	89%	11%
"	"	"	50 nM	8%	22%
"	"	"	100 nM	64%	36%
"	"	"	200 nM	36%	64%
"	"	"	300 nM	25%	75%
14834	29	STOP	25 nM	94%	6%
"	"	"	50 nM	69%	31%
"	"	"	100 nM	65%	35%
"	"	"	200 nM	26%	74%
"	"	"	300 nM	11%	89%
14839	34	3'-UTR	25 nM	140%	---
"	"	"	50 nM	112%	---
"	"	"	100 nM	65%	35%
"	"	"	200 nM	29%	71%
"	"	"	300 nM	22%	78%

EXAMPLE 4: Design and Testing of Chimeric (deoxy gapped) 2'-O-methoxyethyl TNF-α Antisense Oligonucleotides on TNF-α Levels in NeoHK Cells

Oligonucleotides having SEQ ID NO: 28 and SEQ ID NO: 29 were synthesized as uniformly phosphorothioate or mixed phosphorothioate/phosphodiester chimeric oligonucleotides having variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. The sequences and the oligonucleotide chemistries are shown in Table 4. All 2'-MOE cytosines were 5-methyl-cytosines.

Dose response experiments, as discussed in Example 3, were performed using these chimeric oligonucleotides. The effect of the TNF-α antisense oligonucleotides was normalized to the non-specific target control. Results are shown in Table 5. The activities of the chimeric oligonucleotides tested were comparable to the parent phosphorothioate oligonucleotide.

TABLE 4

Nucleotide Sequences of TNF-α Chimeric (deoxy gapped) 2'-O-methoxyethyl Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')[1]	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
14833	AsAsGsTsAsGsAsCsCsTsGsCsCsCsAsGsAsCsTsC	28	2554-2573	coding
16467	**A**o**A**o**G**o**T**o**A**sGsAsCsCsTsGsCsCsCsAs**G**o**A**o**C**o**T**o**C**	28	2554-2573	coding
16468	**A**s**A**s**G**s**T**s**A**sGsAsCsCsTsGsCsCsCsAs**G**s**A**s**C**s**T**s**C**	28	2554-2573	coding
16469	**A**s**A**s**G**s**T**s**A**s**G**sAsCsCsTsGsCsCsCs**A**s**G**s**A**s**C**s**T**s**C**	28	2554-2573	coding
16470	AsAsGsTsAsGsAsCsCsTsGs**C**s**C**s**C**s**A**s**G**s**A**s**C**s**T**s**C**	28	2554-2573	coding
16471	**A**s**A**s**G**s**T**s**A**s**G**s**A**s**C**s**C**sTsGsCsCsCsAsGsAsCsTsC	28	2554-2573	coding
14834	GsGsAsTsGsTsTsCsGsTsCsCsTsCsCsTsCsAsCsA	29	2588-2607	STOP
16472	**G**o**G**o**A**o**T**o**G**sTsTsCsGsTsCsCsTsCsCs**T**o**C**o**A**o**C**o**A**	29	2588-2607	STOP
16473	**G**s**G**s**A**s**T**s**G**sTsTsCsGsTsCsCsTsCsCs**T**s**C**s**A**s**C**s**A**	29	2588-2607	STOP
16474	**G**s**G**s**A**s**T**s**G**s**T**sTsCsGsTsCsCsTsCs**C**s**T**s**C**s**A**s**C**s**A**	29	2588-2607	STOP
16475	**G**s**G**s**A**s**T**s**G**s**T**s**T**s**C**s**G**sTsCsCsTsCsCsTsCsAsCsA	29	2588-2607	STOP
16476	GsGsAsTsGsTsTsCsGsTsCs**C**s**T**s**C**s**C**s**T**s**C**s**A**s**C**s**A**	29	2588-2607	STOP

[1]Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines are 5-methyl-cytidines; "s" linkages are phosphorothioate linkages, "o" linkages are phosphodiester linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 5

Dose Response of NeoHK Cells to TNF-α
Chimeric (deoxy gapped) 2'-O-methoxyethyl Antisense Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
13664	42	Control	50 nM	100%	---
"	"	"	100 nM	100%	---
"	"	"	200 nM	100%	---
"	"	"	300 nM	100%	---
14833	28	Coding	50 nM	69%	31%
"	"	"	100 nM	64%	36%
"	"	"	200 nM	56%	44%
"	"	"	300 nM	36%	64%
16468	28	Coding	50 nM	66%	34%
"	"	"	100 nM	53%	47%
"	"	"	200 nM	34%	66%
"	"	"	300 nM	25%	75%
16471	28	Coding	50 nM	77%	23%
"	"	"	100 nM	56%	44%
"	"	"	200 nM	53%	47%
"	"	"	300 nM	31%	69%
14834	29	STOP	50 nM	74%	26%
"	"	"	100 nM	53%	47%
"	"	"	200 nM	24%	76%
"	"	"	300 nM	11%	89%
16473	29	STOP	50 nM	71%	29%
"	"	"	100 nM	51%	49%
"	"	"	200 nM	28%	72%
"	"	"	300 nM	23%	77%
16476	29	STOP	50 nM	74%	26%
"	"	"	100 nM	58%	42%
"	"	"	200 nM	32%	68%
"	"	"	300 nM	31%	69%

EXAMPLE 5: Design and Testing of Chimeric Phosphorothioate/MMI TNF-α Antisense Oligodeoxynucleotides on TNF-α Levels in NeoHK Cells

Oligonucleotides having SEQ ID NO. 29 were synthesized as mixed phosphorothioate/methylene(methylimino) (MMI) chimeric oligodeoxynucleotides. The sequences and the oligonucleotide chemistries are shown in Table 6. Oligonucleotide 13393 (SEQ ID NO. 49) is an antisense oligonucleotide targeted to the human intracellular adhesion molecule-1 (ICAM-1) and was used as an unrelated target control. All cytosines were 5-methyl-cytosines.

Dose response experiments were performed using these chimeric oligonucleotides, as discussed in Example 3 except quantitation of TNF-α mRNA levels was determined by real-time PER (RT-PER) using the ABI PRISM™ 7700 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a closed-tube, non-gel-based, fluorescence detection system which allows high-throughput quantitation of polymerase chain reaction (PER) products in real-time. As opposed to standard PER, in which amplification products are quantitated after the PER is completed, products in RT-PER are quantitated as they accumulate. This is accomplished by including in the PER reaction an oligonucleotide probe that anneals specifically between the forward and reverse PER primers, and contains two fluorescent dyes. A reporter dye (e.g., JOE or FAM, PE-Applied Biosystems, Foster City, CA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA, PE-Applied Biosystems, Foster City, CA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity of Taq polymerase. During the

extension phase of the PER amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular (six-second) intervals by laser optics built into the ABI PRISM™ 7700 Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

RT-PER reagents were obtained from PE-Applied Biosystems, Foster City, CA. RT-PER reactions were carried out by adding 25 µl PER cocktail (1x TAQMAN7 buffer A, 5.5 mM $MgCl_2$, 300 µM each of dATP, dCTP and dGTP, 600 µM of dUTP, 100 nM each of forward primer, reverse primer, and probe, 20 U RNAse inhibitor, 1.25 units AMPLITAQ GOLD7, and 12.5 U MuLV reverse transcriptase) to 96 well plates containing 25 µl poly(A) mRNA solution. The RT reaction was carried out by incubation for 30 minutes at 48°C. following a 10 minute incubation at 95°C to activate the AMPLITAQ GOLD7, 40 cycles of a two-step PER protocol were carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

For TNF-α the PER primers were:

Forward: 5'-CAGGCGGTGCTTGTTCCT-3' SEQ ID NO. 43

Reverse: 5'-GCCAGAGGGCTGATTAGAGAGA-3' SEQ ID NO. 44 and the PER probe was: FAM-CTTCTCCTTCCTGATCGTGGCAGGC-TAMRA (SEQ ID NO. 45) where FAM or JOE (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye.

For GAPDH the PER primers were:

Forward primer: 5'-GAAGGTGAAGGTCGGAGTC-3' SEQ ID NO. 46

Reverse primer: 5'-GAAGATGGTGATGGGATTTC-3' SEQ ID NO. 47 and the PER probe was: 5' JOE-CAAGCTTCCCGTTCTCAGCC - TAMRA 3' (SEQ ID NO. 48) where FAM or JOE (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye.

Results are shown in Table 7. The oligonucleotide containing MMI linkages was more effective in reducing TNF-α mRNA levels than the uniformly phosphorothioate oligonucleotide. The IC_{50} value was reduced from approximately 75 nM, for oligonucleotide 14834 (SEQ ID NO: 29), to approximately 30 nM for oligonucleotide 16922 (SEQ ID NO: 29).

Dose response experiments were also performed measuring the effect on TNF-α protein levels. Protein levels were measured as described in Example 2. Results are shown in Table 8. The oligonucleotide containing four MMI linkages on each end was more effective in reducing protein levels than the uniformly phosphorothioate oligonucleotide. The IC_{50} value was reduced from approximately 90 nM, for oligonucleotide 14834 (SEQ ID NO: 29), to approximately 45 nM for oligonucleotide 16922 (SEQ ID NO: 29).

TABLE 6

Nucleotide Sequences of Human TNF-α Chimeric Phosphorothioate/MMI Oligodeoxynucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
14834	GsGsAsTsGsTsTsCsGsTsCsCsTsCsCsTsCsAsCsA	29	2588-2607	STOP
16922	GmGmAmTmGsTsTsCsGsTsCsCsTsCsCsTmCmAmCmA	29	2588-2607	STOP
16923	GmGmAmTmGmTmTsCsGsTsCsCsTsCmCmTmCmAmCmA	29	2588-2607	STOP
13393	TsCsTsGsAsGsTsAsGsCsAsGsAsGsGsAsGsCsTsC	49	target control	

[1] All cytosine residues are 5-methyl-cytosines; "s" linkages are phosphorothioate linkages, "m" linkages are methylene(methylimino) (MMI).

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 7

Dose Response of Chimeric Phosphorothioate/MMI TNF-α Antisense Oligodeoxynucleotides on TNF-α mRNA Levels in PMA-Induced NeoHK Cells

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
induced	---	---	---	100%	---
13393	49	control	25 nM	87.3%	12.7%
"	"	"	50 nM	98.5%	1.5%
"	"	"	100 nM	133.1%	---
"	"	"	200 nM	139.6%	---
14834	29	STOP	25 nM	98.7%	1.3%
"	"	"	50 nM	70.8%	29.2%
"	"	"	100 nM	36.0%	64.0%
"	"	"	200 nM	38.2%	61.8%
16922	29	STOP	25 nM	58.9%	41.1%
"	"	"	50 nM	28.2%	71.8%
"	"	"	100 nM	22.2%	77.8%
"	"	"	200 nM	18.9%	81.1%

TABLE 8

Dose Response of Chimeric Phosphorothioate/MMI TNF-α Antisense Oligodeoxynucleotides on TNF-α Protein Levels in PMA-Induced NeoHK Cells

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100.0%	---
13393	49	control	25 nM	117.0%	---
"	"	"	50 nM	86.6%	13.4%
"	"	"	100 nM	98.7%	1.3%
"	"	"	200 nM	78.0%	22.0%

14834	29	STOP	25 nM	84.8%	15.2%
"	"	"	50 nM	76.9%	23.1%
"	"	"	100 nM	44.5%	55.5%
"	"	"	200 nM	18.7%	81.3%
16922	29	STOP	25 nM	67.1%	32.9%
"	"	"	50 nM	48.6%	51.4%
"	"	"	100 nM	20.0%	80.0%
"	"	"	200 nM	7.9%	92.1%
16923	29	STOP	25 nM	79.9%	20.1%
"	"	"	50 nM	69.9%	30.1%
"	"	"	100 nM	56.0%	44.0%
"	"	"	200 nM	44.5%	55.5%

EXAMPLE 6: Additional Human TNF-α Antisense Oligonucleotide Sequences

A second screening of human TNF-α antisense oligonucleotides was performed. Oligonucleotides were designed specifically against specific regions of the TNF-α gene. A series of oligonucleotides was designed to target introns 1 and 3, and exon 4. Sequences targeting introns 1 or 3 were synthesized as uniformly phosphorothioate oligodeoxynucleotides or mixed phosphorothioate/ phosphodiester chimeric backbone oligonucleotides having variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. Sequences targeting exon 4 were synthesized as mixed phosphorothioate/phosphodiester chimeric backbone oligonucleotides having variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. The sequences of the chimeric oligonucleotides are shown in Table 9. Sequences of the uniformly phosphorothioate oligodeoxynucleotides are shown in Table 11. These oligonucleotides were screened at 50 nM and 200 nM for their ability to inhibit TNF-α protein secretion, essentially as described in Example 2. Results for the chimeric backbone oligonucleotides are shown in Table 10; results for the

uniformly phosphorothioate oligodeoxynucleotides are shown in Table 12.

For the chimeric backbone oligonucleotides targeting introns 1 or 3, oligonucleotide 21688 (SED ID NO. 69) gave 60% inhibition or greater. For chimeric backbone oligonucleotides targeting exon 4, two-thirds of the oligonucleotides gave nearly 60% inhibition or greater (SEQ ID NOs. 88, 90, 91, 92, 93, 94, 97, and 98). See Table 10. For the uniformly phosphorothioate oligodeoxynucleotides, five of nine oligonucleotides targeting intron 3 were effective in reducing TNF-α expression by nearly 60% or greater (SEQ ID NOs. 79, 80, 81, 82, and 84). See Table 12.

Oligonucleotides having SEQ ID NO. 91 and SEQ ID NO. 98 were synthesized as a uniformly phosphorothioate oligodeoxynucleotides or mixed phosphorothioate/ phosphodiester chimeric backbone oligonucleotides having variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. The sequences and the oligonucleotide chemistries are shown in Table 13. All 2'-MOE cytosines and 2'-deoxy cytosines were 5-methyl-cytosines.

Dose response experiments, as discussed in Example 3, were performed using these oligonucleotides. Included in this experiment were two oligonucleotides targeting intron 1 and two oligonucleotides targeting intron 3. Results are shown in Tables 14 and 15. The oligonucleotides targeting exon 4 with variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides and/or uniformly 0phosphorothioate or mixed phosphorothioate/phosphodiester were, in general, comparable to the parent compound.

Oligonucleotides targeting introns 1 or 3 having SEQ ID NOs 66, 69 and 80 were effective in reducing TNF-α mRNA levels by greater than 80% and showed a dose response effect with an IC_{50} approximately 110 nM. See Tables 14 and 15.

TABLE 9

Nucleotide Sequences of TNF-α Chimeric Backbone (deoxy gapped) 2'-O-methoxyethyl Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
21669	**T**o**G**o**C**o**G**o**T**sCsTsCsTsCsAsTsTsTsCs**C**o**C**o**C**o**T**o**T**	50	1019-1038	intron 1
21670	**T**o**C**o**C**o**C**o**A**sTsCsTsCsTsCsTsCsCsCs**T**o**C**o**T**o**C**o**T**	51	1039-1058	intron 1
21671	**C**o**A**o**G**o**C**o**G**sCsAsCsAsTsCsTsTsTsCs**A**o**C**o**C**o**C**o**C**o**A**	52	1059-1078	intron 1
21672	**T**o**C**o**T**o**C**o**T**sCsTsCsAsTsCsCsCsTsCs**C**o**C**o**T**o**A**o**T**	53	1079-1098	intron 1
21673	**C**o**G**o**T**o**C**o**T**sTsTsCsTsCsCsAsTsGsTs**T**o**T**o**T**o**T**o**T**	54	1099-1118	intron 1
21674	**C**o**A**o**C**o**A**o**T**sCsTsCsTsTsTsCsTsGsCs**A**o**T**o**C**o**C**o**C**	55	1119-1138	intron 1
21675	**C**o**T**o**C**o**T**o**C**sTsTsCsCsCsCsAsTsCsTs**C**o**T**o**T**o**G**o**C**	56	1139-1158	intron 1
21676	**G**o**T**o**C**o**T**o**C**sTsCsCsAsTsCsTsTsTsCs**C**o**T**o**T**o**C**o**T**	57	1159-1178	intron 1
21677	**T**o**T**o**C**o**C**o**A**sTsGsTsGsCsCsAsGsAsCs**A**o**T**o**C**o**C**o**T**	58	1179-1198	intron 1
21678	**A**o**T**o**A**o**C**o**A**sCsAsCsTsTsAsGsTsGsAs**G**o**C**o**A**o**C**o**C**	59	1199-1218	intron 1
21679	**T**o**T**o**C**o**A**o**T**sTsCsAsTsTsCsAsTsTsCs**A**o**C**o**T**o**C**o**C**	60	1219-1238	intron 1

21680	ToAoToAoTsCsTsGsCsTsTsGsTsTsCsAoToToCoA	61	1239-1258	intron 1
21681	CoToGoToCsTsCsCsAsTsAsTsCsTsTsAoToToToA	62	1259-1278	intron 1
21682	ToCoToCoTsTsCsTsCsAsCsAsCsCsCsCoAoCoAoT	63	1279-1298	intron 1
21683	CoAoCoToTsGsTsTsTsCsTsTsCsCsCsCoCoAoToC	64	1299-1318	intron 1
21684	CoToCoAoCsCsAsTsCsTsTsTsAsTsTsCoAoToAoT	65	1319-1338	intron 1
21685	AoToAoToTsTsCsCsCsGsCsTsCsTsTsToCoToGoT	66	1339-1358	intron 1
21686	CoAoToCoTsCsTsCsTsCsCsTsTsAsGsCoToGoToC	67	1359-1378	intron 1
21687	ToCoToToCsTsCsTsCsCsTsTsAsTsCsToCoCoCoC	68	1379-1398	intron 1
21688	GoToGoToGsCsCsAsGsAsCsAsCsCsCsToAoToCoT	69	1399-1418	intron 1
21689	ToCoToToTsCsCsCsTsGsAsGsTsGsTsCoToToCoT	70	1419-1438	intron 1
21690	AoCoCoToTsCsCsAsGsCsAsTsTsCsAsAoCoAoGoC	71	1439-1458	intron 1
21691	CoToCoCoAsTsTsCsAsTsCsTsGsTsGsToAoToToC	72	1459-1478	intron 1
21692	ToGoAoGoGsTsGsTsCsTsGsGsTsTsTsToCoToCoT	73	1479-1498	intron 1
21693	AoCoAoCoAsTsCsCsTsCsAsGsAsGsCsToCoToToA	74	1871-1890	intron 3
21694	CoToAoGoCsCsCsTsCsCsAsAsGsTsTsCoCoAoAoG	75	1891-1910	intron 3
21695	CoGoGoGoCsTsTsCsAsAsTsCsCsCsCsAoAoAoToC	76	1911-1930	intron 3

21696	AoAoGoToToTsCsTsGsCsCsTsAsCsCsAsToCoAoGoC	77	1931-1950	intron 3
21697	GoToCoCoCoTsTsCsTsCsAsCsAsTsTsGsToCoToCoC	78	1951-1970	intron 3
21698	CoCoToToToCsCsCsTsTsGsAsGsCsTsCsAoGoCoGoA	79	1971-1990	intron 3
21699	GoGoCoCoCoTsGsTsGsCsTsGsTsTsCsCsToCoCoCoAoC	80	1991-2010	intron 3
21700	CoGoToToToCsTsGsAsGsTsAsTsCsCsCsAoCoCoToAoA	81	2011-2030	intron 3
21701	CoAoCoCoAoToTsCsCsCsAsCsCsTsGsGsCsCoAoToGoA	82	2031-2050	intron 3
21702	GoToCoCoCoCoToTsCsTsCsCsTsGsTsCsTsGsTsCoAoToCoC	83	2051-2070	intron 3
21703	CoCoCoAoCoCoCsCsCsAsCsCsAsTsCsCsGsGsGsToToCoCoCoT	84	2071-2090	intron 3
21704	ToCoCoCoToGoGsGsCsCsCsTsCsGsAsGsGsCsToCoCoToGoC	85	2091-2110	intron 3
21705	AoToGoToToCsGsGsTsTsCsAsCsTsCsCsTsCoCoCoAoCoCoA	86	2111-2130	intron 3
21706	AoGoCoAoGoGoGsAsGsAsGsTsCsAsGsGsTsGsToGoGoCoCoC	87	2131-2150	intron 3
21722	GoGoAoToCoCoCsCsAsAsAsGsTsAsGsAsCsCoToGoCoCoC	88	2561-2580	exon 4
21723	CoCoAoGoGoAoCoCsTsCsGsGsGsCsAsAsAsGsTsCoGoGoAoGoA	89	2541-2560	exon 4
21724	ToToAoGoToToCoCsGsGsGsCsCsGsAsTsTsGsAoToCoToToC	90	2521-2540	exon 4

21725	**A**o**G**o**C**o**G**o**C**sTsGsAsGsTsCsGsGsTsCs**A**o**C**o**C**o**C**o**T**	91	2501-2520	exon 4
21726	**T**o**C**o**T**o**C**o**C**sAsGsCsTsGsGsAsAsGsAs**C**o**C**o**C**o**C**o**T**	92	2481-2500	exon 4
21727	**C**o**C**o**C**o**A**o**G**sAsTsAsGsAsTsGsGsGsCs**T**o**C**o**A**o**T**o**A**	93	2461-2480	exon 4
21728	**C**o**C**o**A**o**G**o**G**sGsCsTsTsGsGsCsCsTsCs**A**o**G**o**C**o**C**o**C**	94	2441-2460	exon 4
21729	**C**o**C**o**T**o**C**o**T**sGsGsGsGsTsCsTsCsCsCs**T**o**C**o**T**o**G**o**G**	95	2421-2440	exon 4
21730	**C**o**A**o**G**o**G**o**G**sGsCsTsCsTsTsGsAsTsGs**G**o**C**o**A**o**G**o**A**	96	2401-2420	exon 4
21731	**G**o**A**o**G**o**G**o**A**sGsGsTsTsGsAsCsCsTsTs**G**o**G**o**T**o**C**o**T**	97	2381-2400	exon 4
21732	**G**o**G**o**T**o**A**o**G**sGsAsGsAsCsGsGsCsGsAs**T**o**G**o**C**o**G**o**G**	98	2361-2380	exon 4
21733	**C**o**T**o**G**o**A**o**T**sGsGsTsGsTsGsGsGsTsGs**A**o**G**o**G**o**A**o**G**	99	2341-2360	exon 4

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines and 2'-deoxycytidines are 5-methyl-cytidines; "s" linkages are phosphorothioate linkages, "o" linkages are phosphodiester linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 10

Dose Response of PMA-Induced neoHK Cells to Chimeric Backbone (deoxy gapped) 2'-O-methoxyethyl TNF-α Antisense Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
14834	29	STOP	50 nM	76%	24%
"	"	"	200 nM	16%	84%
21669	50	intron 1	50 nM	134%	---
"	"	"	200 nM	114%	---
21670	51	intron 1	50 nM	122%	---
"	"	"	200 nM	101%	---
21671	52	intron 1	50 nM	90%	10%
"	"	"	200 nM	58%	42%
21672	53	intron 1	50 nM	122%	---
"	"	"	200 nM	131%	---
21673	54	intron 1	50 nM	102%	---
"	"	"	200 nM	110%	---
21674	55	intron 1	50 nM	111%	---
"	"	"	200 nM	96%	4%
21675	56	intron 1	50 nM	114%	---
"	"	"	200 nM	99%	1%
21676	57	intron 1	50 nM	107%	---
"	"	"	200 nM	96%	4%
21677	58	intron 1	50 nM	86%	14%
"	"	"	200 nM	95%	5%
21678	59	intron 1	50 nM	106%	---
"	"	"	200 nM	107%	---
21679	60	intron 1	50 nM	75%	25%
"	"	"	200 nM	73%	27%
21680	61	intron 1	50 nM	76%	24%
"	"	"	200 nM	80%	20%
21681	62	intron 1	50 nM	79%	21%

"	"	"	200 nM	82%	18%
21682	63	intron 1	50 nM	102%	---
"	"	"	200 nM	88%	12%
21683	64	intron 1	50 nM	80%	20%
"	"	"	200 nM	66%	34%
21684	65	intron 1	50 nM	91%	9%
"	"	"	200 nM	69%	31%
21685	66	intron 1	50 nM	98%	2%
"	"	"	200 nM	90%	10%
21686	67	intron 1	50 nM	97%	3%
"	"	"	200 nM	72%	28%
21687	68	intron 1	50 nM	103%	---
"	"	"	200 nM	64%	36%
21688	69	intron 1	50 nM	87%	13%
"	"	"	200 nM	40%	60%
21689	70	intron 1	50 nM	78%	22%
"	"	"	200 nM	74%	26%
21690	71	intron 1	50 nM	84%	16%
"	"	"	200 nM	80%	20%
21691	72	intron 1	50 nM	86%	14%
"	"	"	200 nM	75%	25%
21692	73	intron 1	50 nM	85%	15%
"	"	"	200 nM	61%	39%
21693	74	intron 3	50 nM	81%	19%
"	"	"	200 nM	83%	17%
21694	75	intron 3	50 nM	99%	1%
"	"	"	200 nM	56%	44%
21695	76	intron 3	50 nM	87%	13%
"	"	"	200 nM	84%	16%
21696	77	intron 3	50 nM	103%	---
"	"	"	200 nM	86%	14%
21697	78	intron 3	50 nM	99%	1%
"	"	"	200 nM	52%	48%
21698	79	intron 3	50 nM	96%	4%
"	"	"	200 nM	47%	53%

21699	80	intron 3	50 nM	73%	27%
"	"	"	200 nM	84%	16%
21700	81	intron 3	50 nM	80%	20%
"	"	"	200 nM	53%	47%
21701	82	intron 3	50 nM	94%	6%
"	"	"	200 nM	56%	44%
21702	83	intron 3	50 nM	86%	14%
"	"	"	200 nM	97%	3%
21703	84	intron 3	50 nM	88%	12%
"	"	"	200 nM	74%	26%
21704	85	intron 3	50 nM	69%	31%
"	"	"	200 nM	65%	35%
21705	86	intron 3	50 nM	92%	8%
"	"	"	200 nM	77%	23%
21706	87	intron 3	50 nM	95%	5%
"	"	"	200 nM	82%	18%
21722	88	exon 4	50 nM	81%	19%
"	"	"	200 nM	41%	59%
21723	89	exon 4	50 nM	87%	13%
"	"	"	200 nM	74%	26%
21724	90	exon 4	50 nM	68%	32%
"	"	"	200 nM	33%	67%
21725	91	exon 4	50 nM	55%	45%
"	"	"	200 nM	30%	70%
21726	92	exon 4	50 nM	72%	28%
"	"	"	200 nM	40%	60%
21727	93	exon 4	50 nM	67%	33%
"	"	"	200 nM	40%	60%
21728	94	exon 4	50 nM	62%	38%
"	"	"	200 nM	41%	59%
21729	95	exon 4	50 nM	78%	22%
"	"	"	200 nM	53%	47%
21730	96	exon 4	50 nM	68%	32%
"	"	"	200 nM	48%	52%
21731	97	exon 4	50 nM	77%	23%

"	"	"	200 nM	41%	59%
21732	98	exon 4	50 nM	62%	38%
"	"	"	200 nM	28%	72%
21733	99	exon 4	50 nM	92%	8%
"	"	"	200 nM	74%	26%

TABLE 11

Nucleotide Sequences of Additional Human TNF-α Phosphorothioate Oligodeoxynucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
21804	TGCGTCTCTCATTTCCCCTT	50	1019-1038	intron 1
21805	TCCCATCTCTCTCCCTCTCT	51	1039-1058	intron 1
21806	CAGCGCACATCTTTCACCCA	52	1059-1078	intron 1
21807	TCTCTCTCATCCCTCCCTAT	53	1079-1098	intron 1
21808	CGTCTTTCTCCATGTTTTTT	54	1099-1118	intron 1
21809	CACATCTCTTTCTGCATCCC	55	1119-1138	intron 1
21810	CTCTCTTCCCCATCTCTTGC	56	1139-1158	intron 1
21811	GTCTCTCCATCTTTCCTTCT	57	1159-1178	intron 1
21812	TTCCATGTGCCAGACATCCT	58	1179-1198	intron 1
21813	ATACACACTTAGTGAGCACC	59	1199-1218	intron 1
21814	TTCATTCATTCATTCACTCC	60	1219-1238	intron 1
21815	TATATCTGCTTGTTCATTCA	61	1239-1258	intron 1
21816	CTGTCTCCATATCTTATTTA	62	1259-1278	intron 1
21817	TCTCTTCTCACACCCCACAT	63	1279-1298	intron 1
21818	CACTTGTTTCTTCCCCCATC	64	1299-1318	intron 1
21819	CTCACCATCTTTATTCATAT	65	1319-1338	intron 1
21820	ATATTTCCCGCTCTTTCTGT	66	1339-1358	intron 1
21821	CATCTCTCTCCTTAGCTGTC	67	1359-1378	intron 1
21822	TCTTCTCTCCTTATCTCCCC	68	1379-1398	intron 1
21823	GTGTGCCAGACACCCTATCT	69	1399-1418	intron 1
21824	TCTTTCCCTGAGTGTCTTCT	70	1419-1438	intron 1
21825	ACCTTCCAGCATTCAACAGC	71	1439-1458	intron 1

21826	CTCCATTCATCTGTGTATTC	72	1459-1478	intron 1
21827	TGAGGTGTCTGGTTTTCTCT	73	1479-1498	intron 1
21828	ACACATCCTCAGAGCTCTTA	74	1871-1890	intron 3
21829	CTAGCCCTCCAAGTTCCAAG	75	1891-1910	intron 3
21830	CGGGCTTCAATCCCCAAATC	76	1911-1930	intron 3
21831	AAGTTCTGCCTACCATCAGC	77	1931-1950	intron 3
21832	GTCCTTCTCACATTGTCTCC	78	1951-1970	intron 3
21833	CCTTCCCTTGAGCTCAGCGA	79	1971-1990	intron 3
21834	GGCCTGTGCTGTTCCTCCAC	80	1991-2010	intron 3
21835	CGTTCTGAGTATCCCACTAA	81	2011-2030	intron 3
21836	CACATCCCACCTGGCCATGA	82	2031-2050	intron 3
21837	GTCCTCTCTGTCTGTCATCC	83	2051-2070	intron 3
21838	CCACCCCACATCCGGTTCCT	84	2071-2090	intron 3
21839	TCCTGGCCCTCGAGCTCTGC	85	2091-2110	intron 3
21840	ATGTCGGTTCACTCTCCACA	86	2111-2130	intron 3
21841	AGAGGAGAGTCAGTGTGGCC	87	2131-2150	intron 3

[1] All "C" residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2]Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 12

Dose Response of PMA-Induced neoHK Cells to TNF-α Antisense Phosphorothioate Oligodeoxynucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
14834	29	STOP	50 nM	80%	20%
"	"	"	200 nM	13%	87%
21812	58	intron 1	50 nM	110%	---
"	"	"	200 nM	193%	---
21833	79	intron 3	50 nM	88%	12%
"	"	"	200 nM	8%	92%
21834	80	intron 3	50 nM	70%	30%

"	"	"	200 nM	18%	82%
21835	81	intron 3	50 nM	106%	---
"	"	"	200 nM	42%	58%
21836	82	intron 3	50 nM	71%	29%
"	"	"	200 nM	12%	88%
21837	83	intron 3	50 nM	129%	---
"	"	"	200 nM	74%	26%
21838	84	intron 3	50 nM	85%	15%
"	"	"	200 nM	41%	59%
21839	85	intron 3	50 nM	118%	---
"	"	"	200 nM	58%	42%
21840	86	intron 3	50 nM	120%	---
"	"	"	200 nM	96%	4%
21841	87	intron 3	50 nM	117%	---
"	"	"	200 nM	78%	22%

TABLE 13

Nucleotide Sequences of TNF-α Chimeric (deoxy gapped) 2'-O-Methoxyethyl Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
21725	**A**o**G**o**C**o**G**o**C**sTsGsAsGsTsCsGsGsTsCs**A**o**C**o**C**o**C**o**T**	91	2501-2520	exon 4
25655	**A**s**G**s**C**s**G**sCsTsGsAsGsTsCsGsGsTsCsAs**C**s**C**s**C**s**T**	"	"	"
25656	**A**s**G**s**C**sGsCsTsGsAsGsTsCsGsGsTsCsAsCs**C**s**C**s**T**	"	"	"
25660	**A**o**G**o**C**o**G**sCsTsGsAsGsTsCsGsGsTsCsAs**C**o**C**o**C**o**T**	"	"	"
21732	**G**o**G**o**T**o**A**o**G**sGsAsGsAsCsGsGsCsGsAs**T**o**G**o**C**o**G**o**G**	98	2361-2380	exon 4
25657	**G**s**G**s**T**s**A**sGsGsAsGsAsCsGsGsCsGsAsTs**G**s**C**s**G**s**G**	"	"	"
25658	**G**s**G**s**T**sAsGsGsAsGsAsCsGsGsCsGsAsTsGs**C**s**G**s**G**	"	"	"
25661	**G**o**G**o**T**o**A**sGsGsAsGsAsCsGsGsCsGsAsTs**G**o**C**o**G**o**G**	"	"	"

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines and 2'-deoxycytidines are 5-methyl-cytidines; "s" linkages are phosphorothioate linkages, "o" linkages are phosphodiester linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 14

Dose Response of 20 Hour PMA-Induced neoHK Cells to TNF-α Antisense Oligonucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
14834	29	STOP	75 nM	91.2%	8.8%
"	"	"	150 nM	42.0%	58.0%
"	"	"	300 nM	16.9%	83.1%
21820	66	intron 1	75 nM	79.0%	21.0%
"	"	"	150 nM	34.5%	65.5%
"	"	"	300 nM	15.6%	84.4%
21823	69	intron 1	75 nM	79.5%	20.5%
"	"	"	150 nM	31.8%	68.2%
"	"	"	300 nM	16.2%	83.8%
21725	91	exon 4	75 nM	74.8%	25.2%
"	"	"	150 nM	58.4%	41.6%
"	"	"	300 nM	45.2%	54.8%
25655	91	exon 4	75 nM	112.0%	---
"	"	"	150 nM	55.0%	45.0%
"	"	"	300 nM	39.3%	60.7%
25656	91	exon 4	75 nM	108.3%	---
"	"	"	150 nM	60.7%	39.3%
"	"	"	300 nM	42.8%	57.2%
25660	91	exon 4	75 nM	93.2%	6.8%
"	"	"	150 nM	72.8%	27.2%
"	"	"	300 nM	50.3%	49.7%

TABLE 15

Dose Response of 20 Hour PMA-Induced neoHK Cells to TNF-α Antisense Oligonucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
14834	29	STOP	75 nM	44.9%	55.1%
"	"	"	150 nM	16.3%	83.7%
"	"	"	300 nM	2.2%	97.8%
21834	80	intron 3	75 nM	102.9%	---
"	"	"	150 nM	24.5%	75.5%
"	"	"	300 nM	19.1%	80.9%
21836	82	intron 3	75 nM	70.8%	29.2%
"	"	"	150 nM	55.9%	44.1%
"	"	"	300 nM	32.7%	67.3%
21732	98	exon 4	75 nM	42.4%	57.6%
"	"	"	150 nM	34.9%	65.1%
"	"	"	300 nM	15.4%	84.6%
25657	98	exon 4	75 nM	46.7%	53.3%
"	"	"	150 nM	72.0%	28.0%
"	"	"	300 nM	50.6%	49.4%
25658	98	exon 4	75 nM	83.7%	16.3%
"	"	"	150 nM	56.6%	43.4%
"	"	"	300 nM	36.9%	63.1%
25661	98	exon 4	75 nM	54.9%	45.1%
"	"	"	150 nM	34.4%	65.6%
"	"	"	300 nM	8.6%	91.4%

EXAMPLE 7: Activity of Fully 2'-MOE Modified TNF-α Antisense Oligonucleotides

A series of antisense oligonucleotides were synthesized targeting the terminal twenty nucleotides of each exon at every exon-intron junction of the TNF-α gene. These oligonucleotides were synthesized as fully 2'-methoxyethoxy modified oligonucleotides. The oligonucleotide sequences are shown in Table 16. Oligonucleotide 12345 (SEQ ID NO. 106) is an antisense oligonucleotide targeted to the human intracellular adhesion molecule-1 (ICAM-1) and was used as an unrelated target control.

The oligonucleotides were screened at 50 nM and 200 nM for their ability to inhibit TNF-α mRNA levels, as described in Example 3. Results are shown in Table 17. Oligonucleotide 21794 (SEQ ID NO. 102) showed an effect at both doses, with greater than 75% inhibition at 200 nM.

TABLE 16

Nucleotide Sequences of Human TNF-α Uniform 2'-MOE Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION[3]
21792	**AGGCACTCACCTCTTCCCTC**	100	0972-0991	E1/I1
21793	**CCCTGGGGAACTGTTGGGGA**	101	1579-1598	I1/E2
21794	**AGACACTTACTGACTGCCTG**	102	1625-1644	E2/I2
21795	**GAAGATGATCCTGAAGAGGA**	103	1812-1831	I2/E3
21796	**GAGCTCTTACCTACAACATG**	104	1860-1879	E3/I3
21797	**TGAGGGTTTGCTGGAGGGAG**	105	2161-2180	I3/E4
12345	**GATCGCGTCGGACTATGAAG**	106	target control	

[1] Emboldened residues are 2'-methoxyethoxy residues, 2'-methoxyethoxy cytosine residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

[3] Each target region is an exon-intron junction and is represented in the form, for example, I1/E2, where I, followed by a number, refers to the intron number and E, followed by a number, refers to the exon number.

TABLE 17

Dose Response of neoHK Cells to TNF-α Antisense 2'-MOE Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
induced	---	---	---	100%	---
12345	106	control	50 nM	121%	---
"	"	"	200 nM	134%	---
13393	49	control	50 nM	110%	---
"	"	"	200 nM	112%	---
14834	29	STOP	50 nM	92%	8%
"	"	"	200 nM	17%	83%
21792	100	E1/I1	50 nM	105%	---
"	"	"	200 nM	148%	---
21793	101	I1/E2	50 nM	106%	---
"	"	"	200 nM	172%	---
21794	102	E2/I2	50 nM	75%	25%
"	"	"	200 nM	23%	77%
21795	103	I2/E3	50 nM	79%	21%
"	"	"	200 nM	125%	---
21796	104	E3/I3	50 nM	56%	44%
"	"	"	200 nM	150%	---
21797	105	I3/E4	50 nM	90%	10%
"	"	"	200 nM	128%	---

EXAMPLE 8: Mouse TNF-α Oligonucleotide Sequences

Antisense oligonucleotides were designed to target mouse TNF-α. Target sequence data are from the TNF-α cDNA sequence published by Semon et al. (*Nucleic Acids Res.* **1987**, *15*, 9083-9084); Genbank accession number Y00467, provided herein as SEQ ID NO: 107. Oligonucleotides were synthesized primarily as phosphorothioate oligodeoxynucleotides. Oligonucleotide sequences are shown in Table 18. Oligonucleotide 3082 (SEQ ID NO. 141) is an antisense oligodeoxynucleotide targeted to the human intracellular adhesion molecule-1 (ICAM-1) and was used as an unrelated target control. Oligonucleotide 13108 (SEQ ID NO. 142) is an antisense oligodeoxynucleotide targeted to the herpes simplex virus type 1 and was used as an unrelated target control.

P388D1, mouse macrophage cells (obtained from American Type Culture Collection, Manassas, VA) were cultured in RPMI 1640 medium with 15% fetal bovine serum (FBS) (Life Technologies, Rockville, MD).

At assay time, cell were at approximately 90% confluency. The cells were incubated in the presence of OPTI-MEM7 medium (Life Technologies, Rockville, MD), and the oligonucleotide formulated in LIPOFECTIN7 (Life Technologies), a 1:1 (w/w) liposome formulation of the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-n,n,n-trimethylammonium chloride (DOTMA), and dioleoyl phosphotidylethanolamine (DOPE) in membrane filtered water. For an initial screen, the oligonucleotide concentration was 100 nM in 3 µg/ml LIPOFECTIN7. Treatment was for four hours. After treatment, the medium was removed and the cells were further incubated in RPMI medium with 15% FBS and induced with 10 ng/ml LPS. mRNA was analyzed 2 hours post-induction with PMA.

Total mRNA was isolated using the TOTALLY RNA™ kit (Ambion, Austin, TX), separated on a 1% agarose gel, transferred to HYBOND™-N+ membrane (Amersham, Arlington

Heights, IL), a positively charged nylon membrane, and probed. A TNF-α probe consisted of the 502 bp EcoRI-HindIII fragment from BBG 56 (R&D Systems, Minneapolis, MN), a plasmid containing mouse TNF-α cDNA. A glyceraldehyde 3-phosphate dehydrogenase (G3PDH) probe consisted of the 1.06 kb HindIII fragment from pHcGAP (American Type Culture Collection, Manassas, VA), a plasmid containing human G3PDH cDNA. The fragments were purified from low-melting temperature agarose, as described in Maniatis, T., et al., *Molecular Cloning: A Laboratory Manual*, **1989** and labeled with REDIVUE™ ^{32}P-dCTP (Amersham Pharmacia Biotech, Piscataway, NJ) and PRIME-A-GENE7 labeling kit (Promega, Madison, WI). mRNA was quantitated by a PhosphoImager (Molecular Dynamics, Sunnyvale, CA).

Secreted TNF-α protein levels were measured using a mouse TNF-α ELISA kit (R&D Systems, Minneapolis, MN or Genzyme, Cambridge, MA).

TABLE 18

Nucleotide Sequences of Mouse TNF-α Phosphorothioate Oligodeoxynucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
14846	GAGCTTCTGCTGGCTGGCTG	108	4351-4370	5'-UTR
14847	CCTTGCTGTCCTCGCTGAGG	109	4371-4390	5'-UTR
14848	TCATGGTGTCTTTTCTGGAG	110	4511-4530	AUG
14849	CTTTCTGTGCTCATGGTGTC	111	4521-4540	AUG
14850	GCGGATCATGCTTTCTGTGC	112	4531-4550	coding
14851	GGGAGGCCATTTGGGAACTT	113	5225-5244	junction
14852	CGAATTTTGAGAAGATGATC	114	5457-5476	junction
14853	CTCCTCCACTTGGTGGTTTG	115	5799-5818	junction
14854	CCTGAGATCTTATCCAGCCT	116	6540-6559	3'-UTR
14855	CAATTACAGTCACGGCTCCC	117	6927-6946	3'-UTR

15921	CCCTTCATTCTCAAGGCACA	118	5521-5540	junction
15922	CACCCCTCAACCCGCCCCCC	119	5551-5570	intron
15923	AGAGCTCTGTCTTTTCTCAG	120	5581-5600	intron
15924	CACTGCTCTGACTCTCACGT	121	5611-5630	intron
15925	ATGAGGTCCCGGGTGGCCCC	122	5651-5670	intron
15926	CACCCTCTGTCTTTCCACAT	123	5681-5700	intron
15927	CTCCACATCCTGAGCCTCAG	124	5731-5750	intron
15928	ATTGAGTCAGTGTCACCCTC	125	5761-5780	intron
15929	GCTGGCTCAGCCACTCCAGC	126	5821-5840	coding
15930	TCTTTGAGATCCATGCCGTT	127	5861-5880	coding
15931	AACCCATCGGCTGGCACCAC	128	5891-5910	coding
15932	GTTTGAGCTCAGCCCCCTCA	129	6061-6080	coding
15933	CTCCTCCCAGGTATATGGGC	130	6091-6110	coding
15934	TGAGTTGGTCCCCCTTCTCC	131	6121-6140	coding
15935	CAAAGTAGACCTGCCCGGAC	132	6181-6200	coding
15936	ACACCCATTCCCTTCACAGA	133	6211-6230	STOP
15937	CATAATCCCCTTTCTAAGTT	134	6321-6340	3'-UTR
15938	CACAGAGTTGGACTCTGAGC	135	6341-6360	3'-UTR
15939	CAGCATCTTGTGTTTCTGAG	136	6381-6400	3'-UTR
15940	CACAGTCCAGGTCACTGTCC	137	6401-6420	3'-UTR
15941	TGATGGTGGTGCATGAGAGG	138	6423-6442	3'-UTR
15942	GTGAATTCGGAAAGCCCATT	139	6451-6470	3'-UTR
15943	CCTGACCACTCTCCCTTTGC	140	6501-6520	3'-UTR
3082	TGCATCCCCCAGGCCACCAT	141	target control	
13108	GCCGAGGTCCATGTCGTACGC	142	target control	

[1] All "C" residues are 5-methyl-cytosines except underlined "C" residues are unmodified cytosines; all linkages are phosphorothioate linkages.

[2]Co-ordinates from Genbank Accession No. Y00467, locus name "MMTNFAB", SEQ ID NO. 107.

Results are shown in Table 19. Oligonucleotides 14853 (SEQ ID NO. 115), 14854 (SEQ ID NO. 116), 14855 (SEQ

ID NO. 117), 15921 (SEQ ID NO. 118), 15923 (SEQ ID NO. 120), 15924 (SEQ ID NO. 121), 15925 (SEQ ID NO. 122), 15926 (SEQ ID NO. 123), 15929 (SEQ ID NO. 126), 15930 (SEQ ID NO. 127), 15931 (SEQ ID NO. 128), 15932 (SEQ ID NO. 129), 15934 (SEQ ID NO. 131), 15935 (SEQ ID NO. 132), 15936 (SEQ ID NO. 133), 15937 (SEQ ID NO. 134), 15939 (SEQ ID NO. 136), 15940 (SEQ ID NO. 137), 15942 (SEQ ID NO. 139), and 15943 (SEQ ID NO. 140) gave better than 50% inhibition. Oligonucleotides 15931 (SEQ ID NO. 128), 15932 (SEQ ID NO. 129), 15934 (SEQ ID NO. 131), and 15943 (SEQ ID NO. 140) gave 75% inhibition or better.

TABLE 19

Inhibition of Mouse TNF-α mRNA expression in P388D1 Cells by Phosphorothioate Oligodeoxynucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
Induced	---	---	100%	0%
3082	141	control	129%	---
13664	42	control	85%	15%
14846	108	5'-UTR	84%	16%
14847	109	5'-UTR	88%	12%
14848	110	AUG	60%	40%
14849	111	AUG	75%	25%
14850	112	coding	67%	33%
14851	113	junction	62%	38%
14852	114	junction	69%	31%
14853	115	junction	49%	51%
14854	116	3'-UTR	31%	69%
14855	117	3'-UTR	39%	61%
15921	118	junction	42%	58%
15922	119	intron	64%	36%

15923	120	intron	31%	69%
15924	121	intron	29%	71%
15925	122	intron	30%	70%
15926	123	intron	29%	71%
15928	125	intron	59%	41%
15929	126	coding	38%	62%
15930	127	coding	43%	57%
15931	128	coding	23%	77%
15932	129	coding	25%	75%
15933	130	coding	52%	48%
15934	131	coding	21%	79%
15935	132	coding	39%	61%
15936	133	STOP	35%	65%
15937	134	3'-UTR	45%	55%
15938	135	3'-UTR	76%	24%
15939	136	3'-UTR	33%	67%
15940	137	3'-UTR	38%	62%
15941	138	3'-UTR	54%	46%
15942	139	3'-UTR	42%	58%
15943	140	3'-UTR	25%	75%

EXAMPLE 9: Dose response of antisense phosphorothiaote oligodeoxynucleotide effects on mouse TNF-α mRNA levels in P388D1 cells

Four of the more active oligonucleotides from the initial screen were chosen for dose response assays. These include oligonucleotides 15924 (SEQ ID NO. 121), 15931 (SEQ ID NO. 128), 15934 (SEQ ID NO. 131) and 15943 (SEQ ID NO. 140). P388D1 cells were grown, treated and processed as described in Example 8. LIPOFECTIN7 was added at a ratio of 3 µg/ml per 100 nM of oligonucleotide. The control included LIPOFECTIN7 at a concentration of 6 µg/ml. Results are shown

in Table 20. Each oligonucleotide tested showed a dose response effect with maximal inhibition about 70% or greater and IC_{50} values less than 50 nM.

TABLE 20

Dose Response of LPS-Induced P388D1 Cells to TNF-α Antisense Phosphorothioate Oligodeoxynucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
induced	---	---	---	100%	---
13108	142	control	25 nM	68%	32%
"	"	"	50 nM	71%	29%
"	"	"	100 nM	64%	36%
"	"	"	200 nM	75%	25%
15924	121	intron	25 nM	63%	37%
"	"	"	50 nM	49%	51%
"	"	"	100 nM	36%	64%
"	"	"	200 nM	31%	69%
15931	128	coding	25 nM	42%	58%
"	"	"	50 nM	30%	70%
"	"	"	100 nM	17%	83%
"	"	"	200 nM	16%	84%
15934	131	coding	25 nM	37%	63%
"	"	"	50 nM	26%	74%
"	"	"	100 nM	13%	87%
"	"	"	200 nM	13%	87%
15943	140	3'-UTR	25 nM	38%	62%
"	"	"	50 nM	38%	62%
"	"	"	100 nM	16%	84%
"	"	"	200 nM	16%	84%

EXAMPLE 10: Design and Testing of 2'-O-methoxyethyl (deoxy gapped) TNF-α Antisense Oligonucleotides on TNF-α Levels in P388D1 Cells

Oligonucleotides having SEQ ID NO: 128, SEQ ID NO: 131, and SEQ ID NO: 140 were synthesized as uniformly phosphorothioate oligodeoxynucleotides or mixed phosphorothioate/phosphodiester chimeric oligonucleotides having variable regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. The sequences and the oligonucleotide chemistries are shown in Table 21. All 2'-MOE cytosines were 5-methyl-cytosines.
Oligonucleotides were screened as described in Example 8. Results are shown in Table 22. All the oligonucleotides tested, except oligonucleotide 16817 (SEQ ID NO. 140) showed 44% or greater inhibition of TNF-α mRNA expression. Oligonucleotides 16805 (SEQ ID NO: 131), 16813 (SEQ ID NO: 140), and 16814 (SEQ ID NO: 140) showed greater than 70% inhibition.

TABLE 21

Nucleotide Sequences of Mouse 2'-O-methoxyethyl (deoxy gapped) TNF-α Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
15931	AsAsCsCsCsAsTsCsGsGsCsTsGsGsCsAsCsCsAsC	128	5891-5910	coding
16797	**A**o**A**o**C**o**C**sCsAsTsCsGsGsCsTsGsGsCsAs**C**o**C**o**A**o**C**	"	5891-5910	coding
16798	**A**s**A**s**C**s**C**sCsAsTsCsGsGsCsTsGsGsCsAs**C**s**C**s**A**s**C**	"	5891-5910	coding
16799	**A**o**A**o**C**o**C**o**C**sAsTsCsGsGsCsTsGsGsCs**A**o**C**o**C**o**A**o**C**	"	5891-5910	coding
16800	**A**s**A**s**C**s**C**s**C**sAsTsCsGsGsCsTsGsGsCs**A**s**C**s**C**s**A**s**C**	"	5891-5910	coding
16801	**A**o**A**o**C**o**C**o**C**o**A**o**T**o**C**o**G**sGsCsTsGsGsCsAsCsCsAsC	"	5891-5910	coding
16802	**A**s**A**s**C**s**C**s**C**s**A**s**T**s**C**s**G**sGsCsTsGsGsCsAsCsCsAsC	"	5891-5910	coding
16803	AsAsCsCsCsAsTsCsGsGsCs**T**o**G**o**G**o**C**o**A**o**C**o**C**o**A**o**C**	"	5891-5910	coding
16804	AsAsCsCsCsAsTsCsGsGsCs**T**s**G**s**G**s**C**s**A**s**C**s**C**s**A**s**C**	"	5891-5910	coding
15934	TsGsAsGsTsTsGsGsTsCsCsCsCsCsTsTsCsTsCsC	131	6121-6140	coding
16805	**T**o**G**o**A**o**G**sTsTsGsGsTsCsCsCsCsCsTsTs**C**o**T**o**C**o**C**	"	6121-6140	coding
16806	**T**s**G**s**A**s**G**sTsTsGsGsTsCsCsCsCsCsTsTs**C**s**T**s**C**s**C**	"	6121-6140	coding
16807	**T**o**G**o**A**o**G**o**T**sTsGsGsTsCsCsCsCsCsTs**T**o**C**o**T**o**C**o**C**	"	6121-6140	coding
16808	**T**s**G**s**A**s**G**s**T**sTsGsGsTsCsCsCsCsCsTs**T**s**C**s**T**s**C**s**C**	"	6121-6140	coding
16809	**T**o**G**o**A**o**G**o**T**o**T**o**G**o**G**o**T**sCsCsCsCsCsTsTsCsTsCsC	"	6121-6140	coding

16810	**T**s**G**s**A**s**G**s**T**s**T**s**G**s**G**s**T**sCsCsCsCsCsTsTsCsTsCsC	"	6121-6140	coding
16811	TsGsAsGsTsTsGsGsTsCsCs**C**o**C**o**C**o**T**o**T**o**C**o**T**o**C**o**C**	"	6121-6140	coding
16812	TsGsAsGsTsTsGsGsTsCsCs**C**s**C**s**C**s**T**s**T**s**C**s**T**s**C**s**C**	"	6121-6140	coding
15943	CsCsTsGsAsCsCsAsCsTsCsTsCsCsCsTsTsTsGsC	140	6501-6520	3'-UTR
16813	**C**o**C**o**T**o**G**sAsCsCsAsCsTsCsTsCsCsCsTs**T**o**T**o**G**o**C**	"	6501-6520	3'-UTR
16814	**C**s**C**s**T**s**G**sAsCsCsAsCsTsCsTsCsCsCsTs**T**s**T**s**G**s**C**	"	6501-6520	3'-UTR
16815	**C**o**C**o**T**o**G**o**A**sCsCsAsCsTsCsTsCsCsCsCs**T**o**T**o**T**o**G**o**C**	"	6501-6520	3'-UTR
16816	**C**s**C**s**T**s**G**s**A**sCsCsAsCsTsCsTsCsCsCsCs**T**s**T**s**T**s**G**s**C**	"	6501-6520	3'-UTR
16817	**C**o**C**o**T**o**G**o**A**o**C**o**C**o**A**o**C**sTsCsTsCsCsCsTsTsTsGsC	"	6501-6520	3'-UTR
16818	**C**s**C**s**T**s**G**s**A**s**C**s**C**s**A**s**C**sTsCsTsCsCsCsTsTsTsGsC	"	6501-6520	3'-UTR
16819	CsCsTsGsAsCsCsAsCsTsCs**T**o**C**o**C**o**C**o**T**o**T**o**T**o**G**o**C**	"	6501-6520	3'-UTR
16820	CsCsTsGsAsCsCsAsCsTsCs**T**s**C**s**C**s**C**s**T**s**T**s**T**s**G**s**C**	"	6501-6520	3'-UTR

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines are 5-methyl-cytidines; "s" linkages are phosphorothioate linkages, "o" linkages are phosphodiester linkages, "o" linkages are phosphodiester linkages.

[2]Co-ordinates from Genbank Accession No. Y00467, locus name "MMTNFAB", SEQ ID NO. 107.

TABLE 22

Inhibition of mouse TNF-α mRNA expression in P388D1 Cells by 2'-O-methoxyethyl (deoxy gapped) Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
induced	---	---	100%	0%
13108	142	control	87%	13%
15934	131	coding	28%	72%
16797	128	coding	33%	67%
16798	"	coding	34%	66%
16799	"	coding	56%	44%
16800	"	coding	35%	65%
16801	"	coding	34%	66%
16802	"	coding	38%	62%
16803	"	coding	35%	65%
16804	"	coding	39%	61%
16805	131	coding	29%	71%
16806	"	coding	31%	69%
16807	"	coding	46%	54%
16808	"	coding	43%	57%
16809	"	coding	33%	67%
16810	"	coding	37%	63%
16811	"	coding	40%	60%
16812	"	coding	31%	69%
16813	140	3'-UTR	28%	72%
16814	"	3'-UTR	28%	72%
16815	"	3'-UTR	46%	54%
16816	"	3'-UTR	49%	51%
16817	"	3'-UTR	172%	---
16818	"	3'-UTR	34%	66%

16819	"	3'-UTR	51%	49%
16820	"	3'-UTR	44%	56%

EXAMPLE 11: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Non-Insulin-dependent Diabetes Mellitus

The db/db mouse model, a standard model for non-insulin-dependent diabetes mellitus (NIDDM; Hotamisligil,G.S., et al., Science, **1993**, *259*, 87-90), was used to assess the activity of TNF-α antisense oligonucleotides on blood glucose levels and TNF-α mRNA levels in whole mice. These mice have elevated blood glucose levels and TNF-α mRNA levels compared to wild type mice. Female db/db mice and wild-type littermates were purchased from Jackson Laboratories (Bar Harbor, ME). The effect on oligonucleotide 15931 (SEQ ID NO. 128) on blood glucose levels was determined. For determination of TNF-α mRNA levels, oligonucleotide 15931 (SEQ ID NO. 128), a uniformly modified phosphorothioate oligodeoxynucleotide, was compared to oligonucleotide 25302 (SEQ ID NO. 128), a mixed phosphorothioate/phosphodiester chimeric oligonucleotide having regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides. The sequences and chemistries are shown in Table 23. Oligonucleotide 18154 (SEQ ID NO. 143) is an antisense mixed phosphorothioate/phosphodiester chimeric oligonucleotide, having regions of 2'-O-methoxyethyl (2'-MOE) nucleotides and deoxynucleotides, targeted to the human vascular cell adhesion molecule-1 (VCAM-1) and was used as an unrelated target control.

TABLE 23

Nucleotide Sequence of TNF-α Antisense Oligonucleotide

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
15931	AACCCATCGGCTGGCACCAC	128	5891-5910	coding
25302	**AACCC**ATCGGCTGGC**ACCAC**	128	5891-5910	coding
18154	**TCAAG**CAGTGCCACC**GATCC**	143	target control	

[1] All 2'-methoxyethyl cytosines and 2'-deoxy cytosines residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. Y00467, locus name "MMTNFAB", SEQ ID NO. 107.

db/db mice, six to ten weeks old, were dosed intraperitoneally with oligonucleotide every other day for 2 weeks at 10 mg/kg. The mice were fasted for seven hours prior to administration of the oligonucleotide. The mice were bled via retro orbital sinus every other day, and glucose measurements were performed on the blood. Results are shown in Table 24. Oligonucleotide 15931 (SEQ ID NO. 128) was able to reduce blood glucose levels in db/db mice to levels comparable with wild type mice. Food intake between wild type mice, treated and untreated, did not differ. Food intake between db/db mice, treated and untreated, although higher than wild type mice, did not differ significantly.

Samples of the fat (adipose) tissue from the inguinal fat pads were taken for RNA extraction. RNA was extracted according to *Current Protocols in Molecular Biology*, **1997**, Ausubel, F., et al. ed., John Wiley & Sons. RNA was purified using the RNA clean up procedure of the RNEASY7 Mini kit (Qiagen, Valencia, CA). TNF-α mRNA levels were measured using the RIBOQUANT7 kit (PharMingen, San Diego, CA) with 15 µg of RNA per lane. The probe used was from the mCK-3b Multi-Probe Template set (PharMingen, San Diego,

CA) labeled with [α^{32}P]UTP (Amersham Pharmacia Biotech, Piscataway, NJ). Results are shown in Table 25. Both oligonucleotide 15931 (SEQ ID NO. 128) and 25302 (SEQ ID NO. 128) were able to reduce TNF-α levels in fat, with 25302 (SEQ ID NO. 128) reducing TNF-α to nearly wild-type levels.

TABLE 24

Level of Blood Glucose in Normal and db/db Mice After Treatment with TNF-α Antisense Oligonucleotides

Mouse Strain	ISIS #	SEQ ID NO:	ASO Gene Target	Time (days)	blood glucose (mg/dL)
wild type	---	---	---	1	140
"	15931	128	coding	"	138
db/db	---	---	---	1	260
"	15931	128	coding	"	254
wild type	---	---	---	9	175
"	15931	128	coding	"	163
db/db	---	---	---	9	252
"	15931	128	coding	"	128

TABLE 25

Level of TNF-α mRNA in Fat of db/db Mice After Treatment with TNF-α Antisense Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION
wt saline	---	---	100%
db/db saline	---	---	362%
18154	142	control	130%
15931	128	coding	210%
25302	128	coding	417%

EXAMPLE 12: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Rheumatoid Arthritis

Collagen-induced arthritis (CIA) was used as a murine model for arthritis (Mussener,A., et al., Clin. Exp. Immunol., **1997**, *107*, 485-493). Female DBA/1LacJ mice (Jackson Laboratories, Bar Harbor, ME) between the ages of 6 and 9 weeks were used to assess the activity of TNF-α antisense oligonucleotides. In all studies, 10 mice were used per treatment group.

On day 0, the mice were immunized at the base of the tail with 100 µg of bovine type II collagen which was emulsified in Complete Freund's Adjuvant (CFA). On day 7, a second booster dose of collagen was administered by the same route. On day 14, the mice were injected subcutaneously with 100 µg of LPS. Oligonucleotide was administered intraperitoneally (bolus) three times per week, starting on day 0, for the duration of the 7 week study at the indicated doses. The anti-TNF-α mAb (MM350D, Endogen, Woburn, MA) was administered intraperitoneally at 2 mg/kg once per week, starting on day 0. This antibody was formulated free of preservatives and carrier, and had an endotoxin level of 9.06 EU/mg.

Weights were recorded weekly. Mice were inspected daily for the onset of CIA, characterized by erythema and edema. Upon the onset of the disease, an assessment chart for each animal was started. Paw widths are rear ankle widths of affected and unaffected joints were measured three times a week using a constant tension caliper. Limbs were clinically evaluated and graded on a scale from 0-4, where o=normal, 1=one digit swollen, 2=inflammation present in more than one digit, 3=joint distortion with or without inflammation, and 4=ankylosis as detected by joint manipulation. The progression of all measurements recorded to day 50. On day 50, animals were euthanized by cervical dislocation. All paws were removed and fixed in 10% neutral buffered formalin, from which histopathology slides were prepared.

Arthritis was classified into four stages based on histological evaluation of the degres of inflammation, cartilage damage, pannus formation, bone erosion, osteolysis, fibrosis and ankylosis. Stage I is described by inflammatory cell infiltration in the tissues surrounding the joint and/or superficial layers of the synovium. Stage II is described by pannus formation with damage to the superficial layers of the cartilage. Stage III is described by subchondral bone erosion with some degree of osteoloysis. Stage IV is described by severe destruction of cartilage and bone with areas of fibrosis and/or bony ankylosis. The clinical data was analyzed for differences in the incidence of disease, the onset of disease and the severity of the disease. Descriptive statistics and an analysis of variance (ANOVA) were performed. If a statistically significant difference was detected, a Dunnett's test was performed.

Two independent studies, which differed in dose range, showed that mice treated with ISIS 25302 had a reduced incidence of arthritis (Figures 1A-1B). The two dose ranges were 0.03 to 3.0 mg/kg (low range, Fig. 1A), and 2.5 to 20 mg/kg (high range, Fig. 1B). The lowest incidence of disease was observed in mice treated at doses of 3.0 (22%) and 2.5 mg/kg (38%) of ISIS 25302 respectively, as compared to the vehicle control incidence of 88% in both studies. No further reduction in the incidence of disease occurred in mice treated at higher doses. The onset of disease was delayed in groups treated with ISIS 25302, but varied between experiments (Table 1). The severity of the disease and the percent affected paws were also reduced by treatment with ISIS 25302. Best effects on these clinical outcomes were observed at 3.0 mg/kg in the low dose range study, and 2.5 and 20 mg/kg in the high dose range study.

Treatment of mice with the eight mismatch control, ISIS 30782 (5'**C**ACC**A**A**G**C**T**GC**GG**T**C**CCCA**A** 3'; SEQ ID NO: 502), yielded variable results between the low dose (Table 26A) and high

dose (Table 26B) range studies. In the low dose range study, the one group treated with the control oligonucleotide, at a dose of 3.0 mg/kg, showed comparable improvements in the clinical outcome in comparison to the group treated with the anti-TNF-α oligonucleotide of equivalent dose. In contrast, the eight mismatch control oligonucleotide had minimal effects on the clinical outcome in the high dose range study, at doses of 2.5, 5.0, and 10 mg/kg; but did show effects in the clinic at the highest dose of 20 mg/kg.

TABLE 26A

Treatment	Schedule	Dose (mg/kg)	% incidence	Day of onset	Severity ("SEM)	% affected paws
Vehicle	3x/wk	-	88	18.1"0.7	7.1"2.1	59
ISIS 25302	3x/wk	0.03	70	18.6"1.1	3.1"1.2	28
ISIS 25302	3x/wk	0.1	70	17.6"0.2	3.5"1.5	30
ISIS 25302	3x/wk	0.3	44	21.5"4.5	2.9"1.4	25
ISIS 25302	3x/wk	1.0	67	21.0"3.6	3.4"1.0	36
ISIS 25302	3x/wk	3.0	22	21.5"3.5	1.2"0.8	14
TNF mAb	1x/wk	2.0	30	28.0"1.5	1.3"0.7	8.3
8MM ctrl	3x/wk	3.0	22	17.5"0.5	1.0"0.7	8.3

TABLE 26B

Treatment	Schedule	D o s e (mg/kg)	% incidence	Day of Onset	Severity ("SEM)	% affected paws
Vehicle	3x/wk	-	88	17.6"0.4	6.0"1.6	53
ISIS 25302	3x/wk	2.5	38	28.3"10.8	2.1"1.5	19
ISIS 25302	3x/wk	5.0	50	23.2"5.7	4.5"1.7	40
ISIS 25302	3x/wk	10	44	17.0"0.4	4.0"1.7	33
ISIS 25302	3x/wk	20	56	23.8"5.1	2.2"1.4	19
8MM ctrl	3x/wk	2.5	71	17.4"0.7	6.3"2.2	57
8MM ctrl	3x/wk	5.0	86	20.7"3.1	6.6"2.1	57
8MM ctrl	3x/wk	10	80	18.0"0.6	6.4"1.5	55
8MM ctrl	3x/wk	20	44	19.5"1.6	1.7"1.3	17

In both tables, the incidence is the number of mice with at least one affected paw/total number of mice per group. Severity is the total clinical score/total number of mice in the group. Percent affected paws=(number of affected paws at termination/total number of paws in group) x 100. 8MM ctrl=eight mismatch control (ISIS 30782).

Efficacy of ISIS 25302 (3 mg/kg, three times per week) was found to be comparable to that of an anti-TNF-α mAb (2 mg/kg, once per week) as described in Table 26A. The disease incidence in mice treated with ISIS 25302 was 22% versus 30% for the group treated with the anti-TNF-α mAb. Disease severity and percent affected paws were also reduced to a similar degree in the 3 mg/kg ISIS 25302 and anti-TNF-α mAb treated groups.

Mice treated with the anti-mTNF-α oligonucleotide, ISIS 25302, showed an improvement in the disease outcome when treated three times per week starting on the initial day of collagen-induction. Reduction of symptoms by the ISIS 25302 was dose dependent, and showed equivalent effects when compared to mice treated with an anti-TNF-α monoclonal antibody once per week from the time of collagen-induction. Histological evaluation of the joints showed a reduction in the incidence and severity of arthritic lesions in mice treated with ISIS 25302, but to a lesser extent than those mice treated with the anti-TNF-α mAb.

The efficacy of ISIS 25302 compares favorably to other anti-TNF biological agents which have been evaluated in the "classical" CIA model. For instance, treatment of mice with the recombinant human TNF receptor FC fusion protein prior to onset of disease resulted in a 28% incidence of disease as compared to 86% incidence in the saline control treated animals (Wooley, *J. Immunol.* **151**:6602-6607, 1993). In addition, preventative treatment by an anti-TNF-α antibody in the "classical" model showed 40% reduction in paw swelling in the clinic, as well as reduction in histopathological severity (Williams, *Proc. Natl. Acad. Sci. U.S.A.* **89**:9784-9788, 1992).

A marked difference was observed between the two independent studies of ISIS 25302 in this model of CIA, with respect to responsiveness of the animals to oligonucleotide treatment. Mice were more responsive to oligonucleotide treatment in the low dose range study. This responsiveness was reflected in the histological results, where all oligonucleotide treated groups showed a notable reduction in paw incidence in comparison to the vehicle group. In comparison to the high dose study, mice in the low dose study overall displayed a lower percentage of paws with arthritic changes at the histological level.

In conclusion, evaluation of ISIS 25302 in the accelerated CIA model has shown that an anti-TNF-α oligonucleotide provides an alternative approach to treatment of related human disease indications. Potential advantages of the antisense oligonucleotide therapeutic approach, over the current anti-arthritic (biological) agents, include ease of administration and a lower potential for adverse effects from long term usage.

EXAMPLE 13: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Contact Sensitivity

Contact sensitivity is a type of immune response resulting from contact of the surface of the skin with a sensitizing chemical. A murine model for contact sensitivity is widely used to develop therapies for chronic inflammation, autoimmune disorder, and organ transplant rejection (Goebeler,M., et al., Int Arch. Allergy Appl. Immunol., **1990**, *93*, 294-299). One example of such a disease is atopic dermatitis. Female Balb/c mice between the ages of 8 and 12 weeks are used to assess the activity of TNF-α antisense oligonucleotides in a contact sensitivity model.

Balb/c mice receive injections of oligonucleotide drug in saline via i.v. injection into the tail vein. The abdomen of the mice is shaved using an Oster hair clipper. The animals are anesthetized using isoflurane, and 25 µl of 0.2% 2,4-dinitrofluorobenzene (DNFB) in 4:1 acetone:olive oil is applied

to the shaved abdomen two days in a row. After five days, 10 ml of 0.2% DNFB in the same vehicle is applied to the right ear. After each exposure, the mouse is suspended in air for two minutes to allow the DNFB to absorb into the skin. 24 and 48 hours after application of DNFB to the ear, the ear thickness is measured using a micrometer. Inflammation (dermatitis) is indicated by a ranked thickening of the ear. Thickness of the treated ear is compared to untreated (contralateral) ear thickness.

EXAMPLE 14: Effect of TNF-α Antisense Oligonucleotides in an IL10(-/-) Murine Model for Colitis

The effects of antisense oligonucleotide-inhibition of TNF-α was studied in the IL-$10^{-/-}$ mouse model of colitis. IL10 deficient mice IL-$10^{-/-}$ display some of the features that are observed in Crohn's disease such as discontinuous lesions throughout the gastrointestinal tract and have a cytokine profile that is characteristic of a Th1 immune response. Unlike Crohn's disease, however, IL-$10^{-/-}$ mice show a marked crypt hyperplasia and absence of fissures and fistulas. In addition, IL-$10^{-/-}$ mice have elevated levels of TNF-α expression.

Animals were treated in a prophylactic manner with one of four doses of ISIS 25302 or ISIS. Dosing extended from two weeks of age, before the development of colitis, to eight weeks of age, a time at which IL-$10^{-/-}$ mice typically exhibit advanced stages of colitis. Colitis was assessed by histological evaluation at the conclusion of the study, and the basal and induced secretion of IFN-γ and TNF-α from colon organ culture supernatants was also measured at that time.

Homozygous Interleukin-10 gene-deficient mice, generated on a 129 Sv/Ev background, and 129 Sv/Ev controls were housed under specific pathogen-free conditions. Mice were housed in micro-isolator cages with tight-fitting lids containing spun-polyester fiber filters. Mice were injected every other day with either ISIS 25302 or ISIS 30782 (the 8 mismatch control) at 0.01, 0.1,

1.0, and 10 mg/kg from 2-8 weeks of age via subcutaneous injection.

Animals were sacrificed using sodium pentobarbitol (160 mg/kg). Whole colons were harvested, cut lengthwise, and fixed in 10% phosphate-buffered formalin, paraffin-embedded, sectioned at 4 μm, and stained with haematoxylin and eosin for light microscopic examination. The slides were reviewed independently by a pathologist in a blinded fashion and assigned a histological score for intestinal inflammation (Table 27). The total histological score represents the numerical sum of the four scoring criteria: mucosal ulceration, epithelial hyperplasia, lamina propria mononuclear cell infiltration, and lamina propria neutrophilic infiltration.

TABLE 27

Score	Mucosal ulceration	Epithelial hyperplasia	LP mononuclear infiltration	LP neutrophil infiltrate
0	Normal	Normal	Normal	Normal
1	Surface inflammation	Mild	Slight increase	Slight increase
2	Erosions	Moderate	Marked increase	Marked increase
3	Ulcerations	Pseudopolyps		

Colonic organ cultures were prepared from IL-10 gene-deficient mice treated for six weeks. Due to the patchy nature of colitis in IL-10 gene-deficient mice, whole colons were removed, cut lengthwise, flushed with PBS, and resuspended in tissue culture plates (Falcon 3046; Becton Dickinson Labware, Lincoln Park, NJ) in RPMI-1640 medium supplemented with 10% fetal calf serum, 50 mM 2-mercaptoethanol, penicillin (100 U/mL), and streptomycin (100 U/mL). Cultures were incubated at 37° C in 5% CO_2. After 24 hours in the absence (basal) or presence of 10 μg/mL LPS (*E. coli*, 0111:B4, Sigma), supernatants were harvested and stored at -70° C for analysis of cytokine levels. TNF-α and IFN-γ levels in cell supernatants were measured using ELISA kits purchased from Biosource Cytoscreen (Montreal, Quebec).

Differences between treatment groups were evaluated by analysis of variance (ANOVA). Single arm analysis was performed by the Dunnett's test (SAS Institute Inc., Cary NC).

Over the 6-week treatment period, all treatment groups of IL-10 deficient mice gained weight at a similar rate (data not shown). At 8 weeks of age, IL-$10^{-/-}$ mice displayed a patchy distribution of transmural acute and chronic inflammation, extensive mucosal ulceration, and epithelial hyperplasia. Table 28 shows the histological scores for colon tissue from IL-$10^{-/-}$ mice treated with saline (vehicle), ISIS 25302 or ISIS 30782 (8MM ctrl) from 2 to 8 weeks of age at the indicated doses (n=6). The "total" histological score is the summation of the scores determined for each of the four histological parameters: mucosal ulceration, epithelial hyperplasia, lamina propia (LP) mononuclear cell infiltration, and lamina propria neutrophilic infiltration. Mice receiving the 0.1 mg/kg dose of the anti-TNF-α oligonucleotide, ISIS 25302, demonstrated a marked improvement in their mucosal architecture, which was statistically significant ($p < 0.05$) in comparison to the Vehicle (saline) group (Figure 2). No other group showed a significant histological difference in comparison to Vehicle.

TABLE 28

Treatment	Score	Mucosal ulceration	Mucosal hyperplasia	Mononuclear infiltrate	Neutrophil infiltrate	Total
Saline	**Mean**	**1.00**	**1.83**	**2.00**	**1.83**	**6.67**
	Std. Dev.	0.89	0.41	0.00	0.41	1.21
0.01 mg/kg	**Mean**	**0.50**	**1.50**	**1.50**	**1.50**	**5.00**
ISIS 25302	Std. Dev.	0.55	0.55	0.55	0.55	0.63
0.1 mg/kg	**Mean**	**0.50**	**0.83**	**1.33**	**1.00**	**3.67**
I S I S 25302	Std. Dev.	0.55	0.41	0.52	0.63	0.52
1 mg/kg	**Mean**	**0.67**	**2.00**	**1.67**	**1.67**	**6.00**
ISIS 25302	Std. Dev.	1.21	0.89	0.52	0.52	2.61
10 mg/kg	**Mean**	**1.17**	**1.83**	**1.83**	**1.17**	**6.00**
ISIS 25302	Std. Dev.	1.47	0.98	0.41	0.75	2.83
0.01 mg/kg	**Mean**	**0.83**	**1.83**	**1.33**	**1.67**	**5.67**
8MM ctrl	Std. Dev.	1.17	0.75	0.52	0.52	2.58
0.1 mg/kg	**Mean**	**1.00**	**1.67**	**1.33**	**1.17**	**5.17**

8MM ctrl	Std. Dev.	0.63	0.52	0.52	0.52	0.63
1 mg/kg	**Mean**	**0.67**	**1.67**	**1.33**	**1.33**	**5.00**
8MM ctrl	Std. Dev.	0.52	0.52	0.52	0.52	0.63
10 mg/kg	**Mean**	**0.83**	**2.00**	**1.33**	**1.50**	**5.67**
8 MM ctrl	Std. Dev.	1.17	0.63	0.52	0.55	2.25

Reduction of secreted TNF-α protein levels was observed in colon tissue isolated from mice treated every other day with 0.1 mg/kg of ISIS 25302 under both basal (Figure 3A) and LPS-induced (Figure 3B) conditions. IFN-γ protein secretion from the isolated colon tissue was also reduced in the 0.1 mg/kg ISIS 25302 treated group relative to the saline treated group under both culture conditions (basal, Figure 4A; LPS-induced, Figure 4B). These effects were sequence specific, as the eight base mismatch oligonucleotide at the same dose of 0.1 mg/kg had no effect on basal or LPS-induced TNF-α protein secretion, or LPS-induced IFN-γ secretion.

Although treatment of IL-10$^{-/-}$ mice with an antisense oligonucleotide targeted to TNF-α had no effect on the rate at which these animals gained weight, anti-TNF-α oligonucleotide treatment did have effects on several key disease parameters. Most importantly, antisense treatment at a relatively low dose (0.1 mg/kg) significantly reduced histological signs of colitis in the mice. This included reductions in mucosal ulceration, mucosal hyperplasia, and infiltrations of mononuclear cells and neutrophils into the lamina propria of the colon. These effects were not seen with the eight-base mismatch control oligonucleotide, ISIS 30782, which indicated that the effect was sequence specific.

The histological improvement is most likely due to specific reduction in TNF-α protein levels with antisense treatment. Both the basal and LPS-induced secretion of TNF-α from colons of mice treated with 0.1 mg/kg of ISIS 25302 were reduced, while the control oligonucleotide had no effect. A decrease in basal and induced IFN-γ levels also occurred in the mice treated with 0.1 mg/kg ISIS 25302. Interruption of the proinflammatory cytokine cascade by inhibition of TNF-α expression may have abrogated the recruitment and activation of CD4+ T cells that produce IFN-γ. TNF-α is known to activate expression of key inflammatory intermediates which promote this process, including expression

of cell adhesion molecules, chemokines, and other proinflammatory cytokines (Zhang et al. "Tumor necrosis factor" in *The Cytokine Handbook*, 3rd ed., Academic Press Ltd., pp. 517-547; van Deventer, *Gut* **40**:443-448, 1997).

A biphasic response to the anti-TNF-α oligonucleotide was observed in this genetically engineered mouse model of colitis, where optimal efficacy of the anti-TNF-α oligonucleotide occurred at the mid range dose of 0.1 mg/kg. Treatment at the higher doses of 1.0 and 10 mg/kg resulted in complete loss of efficacy, as observed histologically and by cytokine expression levels. The basis of this response may lie in the undefined roles of the pro- and anti-inflammatory cytokines in the absence of IL-10; and/or the pharmacokinetics and mechanism of action of the oligonucleotide.

In conclusion, ISIS 25302 reduced TNF-α expression levels in a dose and sequence-dependent manner in the IL-10 deficient mice. Specific reduction of this proinflammatory molecule diminished the pathological features associated with the intestinal injury and inflammation which occurs in the absence of IL-10 in these mice. The results from this mouse model of colitis indicate that antisense oligonucleotides to TNF-α represent a new treatment of Crohn's disease in man.

EXAMPLE 15: Effect of TNF-α Antisense Oligonucleotides in a DSS-induced Murine Model for Colitis

The pathological features of DSS-induced colitis in mice are similar in many respects to human ulcerative colitis (UC) (Table 29). This model is characterized by ulceration, epithelial damage, mucosal or transmural inflammatory infiltrate, and lymphoid hyperplasia of the colon. These effects are attributed to inappropriate macrophage function, alterations of the lumina bacteria, and the direct toxic effects of DSS on the colonic epithelium (Okayasu, *Gastroenterol.* **98**:694-702, 1990). Both acute and chronic colitis may be studied in this model, by alteration of the DSS administration schedule (Okayasu, 1990,

supra.; Cooper et al., *Lab. Invest.* **69**:238-249, 1993). The efficacy of an anti-TNF-α mAb has been shown in both the acute and chronic model of DSS-induced colitis (Murthy et al., *Aliment. Pharmacol. Ther.* **13**:251-260, 1999; Kojougaroff et al., *Clin. Exp. Immunol.* **107**:353-358, 1997), as well as efficacy of an antisense oligonucleotide to ICAM-1 in the acute model of DSS-induced colitis (Bennett et al., *J. Pharmacol. Exp. Ther.* **280**:988-1000, 1997).

TABLE 29

Feature	Crohn's	Ulcerative colitis	DSS-induced colitis
Location	GI tract	Colon	Colon
Depth	Transmural	Mucosal	Mucosal
Extent	Discontinuous	Continuous	Continuous
Symptoms	Non-bloody diarrhea, fistula	Bloody diarrhea, no fistula	BD, no fistula
Granuloma	Yes	No	No
Genetic	Yes	Yes	Yes
Microbial	Yes	Yes	Yes
Immunological	Yes	Yes	Yes
Inflammation	Transmural	Epithelium	Epithelium
TNF-α	Elevated	Elevated	Elevated

ISIS 25302 was evaluated for efficacy in both the acute and chronic models of DSS-induced colitis. ISIS 25302 is similar in design to the human anti-TNF-α oligonucleotide, ISIS 104838, with respect to the phosphorothioate modified backbone, methylated cytosine residues, and modification of each of the five 5' and 3' sugar residues with 2'-O-(2-methoxyethyl).

Female Swiss-Webster mice, 7 to 8 weeks of age weighing 25 to 30 grams, were obtained from Taconic or Jackson Laboratory. The animals were housed at 22°C and 12 hours of dark and light cycles. Mouse chow and water were made available *ab libitum*.

Female Swiss-webster mice (n = 2) were intravenously injected with 20 mg/kg of ISIS 13920 in saline or with saline alone on day 1, 3, and 5 of the acute DSS-induced colitis protocol as described below. ISIS 13920 is a fully modified

phosphorothioate oligodeoxynucleotide, 5′ TCCGTCATCGCTCCTCAGGG 3′ (SEQ ID NO: 503), with 2′-O-(2-methoxyethyl) modified indicated by underline. This oligonucleotide is directed to the human ras-Ha gene. Two additional groups (n = 2) of normal mice (no DSS) were subjected to the same oligonucleotide administration protocol. Mice were sacrificed on day 7. Colons were removed, trimmed longitudinally, fixed in 10% neutral buffered formaldehyde, and processed through paraffin. Four micron sections were cut from paraffin-embedded tissues, and deparaffinized by standard histological procedures. Endogenous tissue peroxidase activity was quenched with Peroxidase Blocking Reagent (DAKO; Carpenteria, CA) for 10 min at room temperature (r.t.). Tissue was treated with proteinase K (DAKO) for 10 min at r.t. to make it permeable for staining. After blocking with normal donkey serum (Jackson Laboratory; Bar Harbor, Maine), the sections were incubated for 45 min at r.t. with the 2E1-B5 anti-oligonucleotide mAb (Butler et al., *Lab. Invest.*, **77**:379-388, 1997). Sections were rinsed with PBS and then incubated with peroxidase conjugated rabbit anti-mouse IgG1 (Zymed Laboratories; San Francisco, CA) diluted 1:200 for 30 min at r.t. Slides were washed thoroughly with PBS and then stained for peroxidase activity by addition of 3,3′-diamino-benzidine (DAKO) for 5 min at r.t.

Mice received 4% dextran sodium sulfate (MW 40,000, ICN Biomedicals, Inc., Aurora OH) in double distilled water *ad libitum* from day 0 until day 5 to induce colitis. On day 5, the 4% DSS was replaced with plain drinking water.

Mice were first weighed and randomized into groups of seven or eight animals. Mice were administered oligonucleotide every other day (q2d) by i.v. or s.c. injection at the indicated doses from day -2 to day 6. The vehicle group was administered 1 mL/kg 0.9% saline (Baxter Healthcare Corporation, Deerfield, Illinois) under a similar treatment protocol.

Disease activity index was calculated on day 7 based on the summation of the weight, hemoccult, and stool consistency scores

(Table 30). Mice were weighed initially on day 0, and then every day beginning on day 3 until time of sacrifice. The stool consistency from each mouse was evaluated daily by visible appearance, beginning on day 3. On the day of sacrifice, day 7, stool from each mouse was evaluated for occult blood using the Hemoccult test (SmithKline Diagnostics, Inc., San Jose CA). After sacrifice, the colon was removed from the ileocecal junction to the anal verge. The entire colon was then measured and observed for gross changes in the appearance of the mucosa, the total length of the colon was noted, and sections of the colon were dissected for histopathological evaluation.

TABLE 30

Score	Weight loss	Stool consistency	Hemoccult
0	None	Normal	Negative
1	1-5%		
2	6-10%	Loose stool	Positive
3	11-15%		
4	>15%	Diarrhea	Gross bleeding

Mice were first weighed and randomized into groups of eight to ten animals. Chronic colitis was induced by giving the mice 4% DSS in their drinking water for two cycles. For each cycle, DSS was administered until the disease activity index (DAI) reached a score of 2.0 to 2.5 (see scoring criteria below) in at least one group, at which time the 4% DSS was replaced with plain drinking water. The first cycle of DSS administration was followed by 14 days of plain drinking water. The second cycle of DSS was followed by 8 to 9 days of plain drinking water, at which time the mice were sacrificed.

Oligonucleotide was administered subcutaneously (s.c.) for four consecutive days starting on the second day of the first cycle, and then every other day thereafter at doses of 0.25 mg/kg, 2.5 mg/kg, and 12.5 mg/kg; or 0.5 and 2.5 mg/kg. TNF-α mAb was administered s.c. one time at the beginning of each cycle for a total of two treatments at 30 µg/mouse.

Chronic colitis progression was determined by daily measurement of the Disease Activity Index (DAI), consisting of weight loss, stool consistency and hemoccult scores (Cooper et al., 1993, *supra*.). Each parameter was given a score (Table 30) and the combined score was divided by three to obtain the disease activity index (DAI). This method has been shown to correlate with the histological measures of inflammation and crypt damage.

The damage to the crypts and extent of recovery were determined by histological analysis of the proximal and distal sections of the colon based on the crypt grade and percent involvement in each section. Crypt grades were scored as Grade 0 = intact crypt; Grade 1= loss of 1/3 crypt; Grade 2 = loss of 2/3 of crypt; Grade 3 = loss of entire crypt w/intact epithelium; and Grade 4 = loss of entire crypt w/loss of epithelium (ulceration). Percent involvement was scored as 1 = 1-25%; 2 = 26-50%; 3 = 51-75%; and 4 = 76-100%. Total crypt score is the combined scores of the distal and proximal colon sections. The inflammation score is the product of the grade of inflammation and the extent of involvement, where Grade 0 = normal; Grade 1 = mild; Grade 2 = moderate; Grade 3 = Severe; and Percent Involvement 1 = 1-25%; 2 = 26-50%; 3 = 51-75%; 4 = 76-100%.

Total RNA was isolated from a 1 mm full length colon strip from each animal using the RNeasy Mini Kit (Qiagen, Valencia CA). Mouse TNF-α and G3PDH mRNA levels were determined by standard northern blot procedures. TNF-α probe signals were normalized to G3PDH probe signal.

Differences between treatment groups were evaluated by analysis of variance (ANOVA). If a statistically significant difference was detected by ANOVA then the Dunnett's test was applied (SAS Institute Inc., Cary NC).

Previous studies have examined the distribution of the "first-generation" phosphorothioate oligodeoxynucleotides in colon tissue of normal and DSS-treated mice, and demonstrated localization of oligonucleotide in both the lamina propia and the epithelial cells of the mucosal layer (Bennett, 1997, *supra*.).

In this case, differences were observed between the two groups of mice with respect to degree of tissue accumulation as well as relative distribution between the lamina propia and epithelial cells. Disruption of the epithelial mucosa layer and influx of immune cells into the lamina propia in the DSS-treated mice coincided with increased accumulation of the oligonucleotide in the tissue, particularly in the epithelial layer.

To obtain information on the localization of a 2'-O-(2-methoxyethyl) modified (2'-MOE) phosphorothioate oligodeoxynucleotide a similar experiment was performed using immunohistochemical staining techniques, instead of autoradiographic or fluorescent techniques, to detect the oligonucleotide (Butler et al., 1997, *supra*.) in the colon tissue. Immunohistochemical staining allows for direct detection of the oligonucleotide without further labeling steps during oligonucleotide synthesis. The previously identified anti-oligonucleotide monoclonal antibody, 2E1, was utilized for this purpose (Butler, 1997, *supra*.). Cumulative studies have shown that the strength of the signal obtained from histological staining of an oligonucleotide with the 2E1 antibody is dependent on the oligonucleotide sequence. In this respect, the staining signal for ISIS 25302 proved to be modest. For this reason we utilized ISIS 13920, a 2'-MOE modified phosphorothioate oligodeoxynucleotide with enhanced histological staining properties, to evaluate the distribution of this type of oligonucleotide in colon tissue of normal and DSS-treated mice. A similar distribution and accumulation profile was observed with the "second-generation" 2'-MOE modified phosphorothioate oligodeoxynucleotide, as had previously been observed for a rhodamine labeled "first-generation" phosphorothioate oligodeoxynucleotide (Bennett, 1997, *supra*.). Enhanced staining by the anti-oligonucleotide antibody, 2E1, was observed in the colon tissue of DSS-treated mice, in comparison to the normal mice.

Mice treated with ISIS 25302 every other day at a dose of 1 mg/kg in the acute model of DSS-induced colitis showed a 44% reduction in the disease activity index (DAI) relative to the saline treated control group (1.4±0.2 vs 2.6±0.2; Fig 5A). In comparison, mice treated one time with 25 micrograms of the anti-TNF-α mAb, at the commencement of DSS-induction, showed a 57 % reduction in the DAI. In both cases, the reduction in DAI was significant ($p < 0.05$) in comparison to the saline treated group. In contrast to the other two treatments, mice treated with 50 micrograms of antibody showed no improvement in the DAI. Improvement in the DAI correlated with an increase in colon length (Fig 5B). The mean colon length of the saline treated DSS-induced mice was 57% the length of normal mice (see also Okayasu, 1990, *supra.*), whereas those of the ISIS 25302 and anti-TNF-α antibody (25µg) treated mice were 76% and 79% respectively. The mean colon lengths of each of the two anti-TNF-α treated groups were significantly different from both the saline treated DSS-induced mice and normal mice ($p < 0.05$).

The effect of ISIS 25302 on the development of acute colitis was dose and sequence dependent (Fig. 6A-6B). A reduction of the clinical symptoms of DSS-induced colitis, as measured by the DAI, was observed in mice treated with 0.04 (60%), 0.2 (60%), and 1 mg/kg (80%) of ISIS 25302 relative to saline treated control mice. Mice treated with the eight base mismatch control oligonucleotide, ISIS 30782, showed no reduction in the DAI in comparison to the saline treated group. The reduction in DAI in mice treated with ISIS 25302 at 0.04, 0.2, and 1.0 mg/kg was statistically significant in comparison to mice treated with the eight base mismatch control oligonucleotide at 1.0 mg/kg ($p < 0.05$). A statistically significant difference was also observed between the 1.0 mg/kg ISIS 25302 group and the saline treated group. Treatment of the mice with ISIS 25302 at the higher dose of 5 mg/kg, yielded no improvement in the DAI; as previously observed in mice treated with 50 micrograms of the anti-TNF-α mAb (described below). A partial loss of efficacy was also observed

in the acute DSS-induced colitis model with the anti-ICAM-1 oligonucleotide, ISIS 3082, at a dose of 5 mg/kg (Bennett, 1997, *supra*.). In the ICAM-1 study mice were administered oligonucleotide once a day for five consecutive days, instead of every other day for a total of five injections. Loss of efficacy, in all applications, may have resulted from an excessive accumulation of the oligonucleotide (or antibody) in the inflamed tissue, which in turn had an adverse effect on the animals (immune) response to intestinal injury by DSS.

ISIS 25302 was also tested for efficacy in the chronic model of DSS-induced mouse colitis. In this model, DSS was administered a second time, fourteen days after the first period of DSS administration. Animals were treated with ISIS 25302 prior to establishment of disease, starting on Day 2 of the first cycle of DSS administration. A dose-dependent reduction in the clinical signs of chronic colitis was observed in the mice treated with ISIS 25302 (Fig 7A). For example, a 49% reduction (0.88 ± 0.17) in the disease activity index (DAI) was observed in mice treated at the lowest dose of 0.25 mg/kg of ISIS 25302, in comparison to the saline treated control group (1.7 ± 0.3) at the end of the second cycle (Day 10, Fig 7B). A greater reduction in the DAI, 86 to 87%, was observed in mice treated at the higher doses of 2.5 and 12.5 mg/kg of ISIS 25302 (0.22 ± 0.11 and 0.27 ± 0.11, respectively). In comparison, animals treated with the anti-TNF-α mAb showed a 61% reduction in DAI (0.67 ± 0.14). At this time the reductions in DAI scores were statistically significant ($p < 0.05$) in mice treated with either the anti-TNF-α mAb or ISIS 25302, at all three doses, in comparison to the vehicle group.

Mice that showed an improvement in DAI also showed a reduction in inflammatory infiltrates and crypt damage at the histological level as compared to the untreated and vehicle groups (Fig. 8A-B). For example, mice treated with ISIS 25302 at 2.5 and 12.5 mg/kg demonstrated a 43% and 52% reduction in total inflammatory infiltrates (respectively), and a 43% and 48%

reduction in total crypt damage relative to vehicle (Fig 8A). The proximal region of the colon was more responsive to treatment by ISIS 25302, than the distal region (Fig 8B). However, the severity of the disease was greater in the distal region of the colon.

Although not statistically significant, a thirty percent reduction in target TNF-α mRNA levels was observed in the colon tissue of mice treated at the higher doses of 2.5 and 12.5 mg/kg ISIS 25302 (Fig. 9). The TNF-α mRNA levels in colons from mice treated at the lower dose of 0.25 mg/kg of ISIS 25302 were not reduced in comparison to the vehicle group. The reduced levels of TNF-α mRNA observed for mice treated with the two higher doses of ISIS 25302 supports the dose-dependent response observed in the clinic, as measured by the DAI.

The anti-mTNF-α oligoncucleotide, ISIS 25302, showed dose and sequence-specific efficacy in both the acute and chronic indications of DSS-induced colitis. ISIS 25302 treatment was also comparable in effect to treatment with an anti-TNF mAb in both indications. The reduction in the clinical symptoms observed in DSS-induced mice treated with ISIS 25302 correlated with a reduction of inflammatory infiltrates and crypt damage. Target TNF-α mRNA levels were also reduced in colon tissue derived from DSS-induced animals treated with ISIS 25302, relative to vehicle controls. The efficacy of ISIS 25302 in both the acute and chronic models of DSS-induced mouse colitis indicates that an antisense oligonucleotide which targets TNF-α mRNA represents a novel approach for treatment of human inflammatory bowel disease.

EXAMPLE 16: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Crohn's Disease

C3H/HeJ, SJL/JK and IL10-/- mice are used in a TNBS (2,4,5,-trinitrobenzene sulfonic acid) induced colitis model for Crohn's disease (Neurath,M.F., et al., J. Exp. Med., **1995**, *182*, 1281-1290). Mice between the ages of 6 weeks and 3 months are used to assess the activity of TNF-α antisense oligonucleotides.

C3H/HeJ, SJL/JK and IL10-/- mice are fasted overnight prior to administration of TNBS. A thin, flexible polyethylene tube is slowly inserted into the colon of the mice so that the tip rests approximately 4 cm proximal to the anus. 0.5 mg of the TNBS in 50% ethanol is slowly injected from the catheter fitted onto a 1 ml syringe. Animals are held inverted in a vertical position for approximately 30 seconds. TNF-α antisense oligonucleotides are administered either at the first sign of symptoms or simultaneously with induction of disease. Animals, in most cases, are dosed every day. Administration is by i.v., i.p., s.q., minipumps or intracolonic injection. Experimental tissues are collected at the end of the treatment regimen for histochemical evaluation.

EXAMPLE 17: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Multiple Sclerosis

Experimental autoimmune encephalomyelitis (EAE) is a commonly accepted murine model for multiple sclerosis (Myers,K.J., et al., J. Neuroimmunol., **1992**, *41*, 1-8). SJL/H, PL/J, (SJLxPL/J)F1, (SJLxBalb/c)F1 and Balb/c female mice between the ages of 6 and 12 weeks are used to test the activity of TNF-α antisense oligonucleotides.

The mice are immunized in the two rear foot pads and base of the tail with an emulsion consisting of encephalitogenic protein or peptide (according to Myers,K.J., et al., J. of Immunol., **1993**, *151*, 2252-2260) in Complete Freund's Adjuvant supplemented with heat killed Mycobacterium tuberculosis. Two days later, the mice receive an intravenous injection of 500 ng Bordatella pertussis toxin and additional adjuvant.

Alternatively, the disease may also be induced by the adoptive transfer of T-cells. T-cells are obtained from the draining of the lymph nodes of mice immunized with encephalitogenic protein or peptide in CFA. The T cells are grown in tissue culture for several days and then injected intravenously into naive syngeneic recipients.

Mice are monitored and scored daily on a 0-5 scale for signals of the disease, including loss of tail muscle tone, wobbly gait, and various degrees of paralysis.

EXAMPLE 18: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Pancreatitis

Swiss Webster, C57BL/56, C57BL/6 lpr and gld male mice are used in an experimental pancreatitis model (Niederau,C., et al., Gastroenterology, **1985**, *88*, 1192-1204). Mice between the ages of 4 and 10 weeks are used to assess the activity of TNF-α antisense oligonucleotides.

Caerulin (5-200 μg/kg) is administered i.p. every hour for one to six hours. At varying time intervals, the mice are given i.p. injection of avertin and bled by cardiac puncture. The pancreas and spleen are evaluated for histopathology and increased levels of IL-1β, IL-6, and TNF-α. The blood is analyzed for increased levels of serum amylase and lipase. TNF-α antisense oligonucleotides are administered by intraperitoneal injection at 4 hours pre-caerulin injections.

EXAMPLE 19: Effect of TNF-α Antisense Oligonucleotides in a Murine Model for Hepatitis

Concanavalin A-induced hepatitis is used as a murine model for hepatitis (Mizuhara,H., et al., J. Exp. Med., **1994**, *179*, 1529-1537). It has been shown that this type of liver injury is mediated by Fas (Seino,K., et al., Gastroenterology **1997**, 113, 1315-1322). Certain types of viral hepatitis, including Hepatitis C, are also mediated by Fas (*J. Gastroenterology and Hepatology*, **1997**, *12*, S223-S226). Female Balb/c and C57BL/6 mice between the ages of 6 weeks and 3 months are used to assess the activity of TNF-α antisense oligonucleotides.

Mice are intravenously injected with oligonucleotide. The pretreated mice are then intravenously injected with 0.3 mg concanavalin A (Con A) to induce liver injury. Within 24 hours following Con A injection, the livers are removed from the

animals and analyzed for cell death (apoptosis) by *in vitro* methods. In some experiments, blood is collected from the retro-orbital vein.

EXAMPLE 20: Effect of Antisense Oligonucleotide Targeted to TNF-α on Survival in Murine Heterotopic Heart Transplant Model

To determine the therapeutic effects of TNF-α antisense oligonucleotides in preventing allograft rejection, murine TNF-α-specific oligonucleotides are tested for activity in a murine vascularized heterotopic heart transplant model. Hearts from Balb/c mice are transplanted into the abdominal cavity of C3H mice as primary vascularized grafts essentially as described by Isobe et al., *Circulation* **1991**, 84, 1246-1255. Oligonucleotide is administered by continuous intravenous administration via a 7-day Alzet pump. The mean survival time for untreated mice is usually approximately 9-10 days. Treatment of the mice for 7 days with TNF-α antisense oligonucleotides is expected to increase the mean survival time.

EXAMPLE 21: Optimization of Human TNF-α Antisense Oligonucleotide

Additional antisense oligonucleotides targeted to intron 1 of human TNF-α were designed. These are shown in Table 31. Oligonucleotides are screened by RT-PCR as described in Example 5 hereinabove.

TABLE 31

Nucleotide Sequences of Human TNF-α Intron 1 Antisense Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
100181	**AG**TGTCTTCTGTGTGCCA**GA**	144	1409-1428	intron 1
100201	**AG**TGTCTTCTGTGTGC**CAGA**	"	"	intron 1
100230	**AGTG**TCTTCTGTGTGCCA**GA**	"	"	intron 1
100250	**AGTG**TCTTCTGTGTGC**CAGA**	"	"	intron 1
100182	**GT**GTCTTCTGTGTGCCAG**AC**	145	1408-1427	intron 1
100202	**GT**GTCTTCTGTGTGCC**AGAC**	"	"	intron 1
100231	**GTGT**CTTCTGTGTGCCAG**AC**	"	"	intron 1
100251	**GTGT**CTTCTGTGTGCC**AGAC**	"	"	intron 1
100183	**TG**TCTTCTGTGTGCCAGA**CA**	146	1407-1426	intron 1
100203	**TG**TCTTCTGTGTGCCA**GACA**	"	"	intron 1
100232	**TGTC**TTCTGTGTGCCAGA**CA**	"	"	intron 1
100252	**TGTC**TTCTGTGTGCCA**GACA**	"	"	intron 1
100184	**GT**CTTCTGTGTGCCAGAC**AC**	147	1406-1425	intron 1
100204	**GT**CTTCTGTGTGCCAG**ACAC**	"	"	intron 1
100233	**GTCT**TCTGTGTGCCAGAC**AC**	"	"	intron 1
100253	**GTCT**TCTGTGTGCCAG**ACAC**	"	"	intron 1
100185	**TC**TTCTGTGTGCCAGACA**CC**	148	1405-1424	intron 1
100205	**TC**TTCTGTGTGCCAGA**CACC**	"	"	intron 1
100234	**TCTT**CTGTGTGCCAGACA**CC**	"	"	intron 1
100254	**TCTT**CTGTGTGCCAGA**CACC**	"	"	intron 1
100186	**CT**TCTGTGTGCCAGACAC**CC**	149	1404-1423	intron 1
100206	**CT**TCTGTGTGCCAGAC**ACCC**	"	"	intron 1
100235	**CTTC**TGTGTGCCAGACAC**CC**	"	"	intron 1
100255	**CTTC**TGTGTGCCAGAC**ACCC**	"	"	intron 1
100187	**TT**CTGTGTGCCAGACACC**CT**	150	1403-1422	intron 1
100207	**TT**CTGTGTGCCAGACA**CCCT**	"	"	intron 1

100236	**TTCT**GTGTGCCAGACACC**CT**	"	"	intron 1
100256	**TTCT**GTGTGCCAGACA**CCCT**	"	"	intron 1
100188	**TC**TGTGTGCCAGACACCC**TA**	151	1402-1421	intron 1
100208	**TC**TGTGTGCCAGACAC**CCTA**	"	"	intron 1
100237	**TCTG**TGTGCCAGACACCC**TA**	"	"	intron 1
100257	**TCTG**TGTGCCAGACAC**CCTA**	"	"	intron 1
100189	**CT**GTGTGCCAGACACCCT**AT**	152	1401-1420	intron 1
100209	**CT**GTGTGCCAGACACC**CTAT**	"	"	intron 1
100238	**CTGT**GTGCCAGACACCCT**AT**	"	"	intron 1
100258	**CTGT**GTGCCAGACACC**CTAT**	"	"	intron 1
100190	**TG**TGTGCCAGACACCCTA**TC**	153	1400-1419	intron 1
100210	**TG**TGTGCCAGACACCC**TATC**	"	"	intron 1
100239	**TGTG**TGCCAGACACCCTA**TC**	"	"	intron 1
100259	**TGTG**TGCCAGACACCC**TATC**	"	"	intron 1
100191	**TG**TGCCAGACACCCTATC**TT**	154	1398-1417	intron 1
100211	**TG**TGCCAGACACCCTA**TCTT**	"	"	intron 1
100240	**TGTG**CCAGACACCCTATC**TT**	"	"	intron 1
100260	**TGTG**CCAGACACCCTA**TCTT**	"	"	intron 1
100192	**GT**GCCAGACACCCTATCT**TC**	155	1397-1416	intron 1
100212	**GT**GCCAGACACCCTAT**CTTC**	"	"	intron 1
100241	**GTGC**CAGACACCCTATCT**TC**	"	"	intron 1
100261	**GTGC**CAGACACCCTAT**CTTC**	"	"	intron 1
100193	**TG**CCAGACACCCTATCTT**CT**	156	1396-1415	intron 1
100213	**TG**CCAGACACCCTATC**TTCT**	"	"	intron 1
100242	**TGCC**AGACACCCTATCTT**CT**	"	"	intron 1
100262	**TGCC**AGACACCCTATC**TTCT**	"	"	intron 1
100194	**GC**CAGACACCCTATCTTC**TT**	157	1395-1414	intron 1
100214	**GC**CAGACACCCTATCT**TCTT**	"	"	intron 1
100243	**GCCA**GACACCCTATCTTC**TT**	"	"	intron 1
100263	**GCCA**GACACCCTATCT**TCTT**	"	"	intron 1
100195	**CC**AGACACCCTATCTTCT**TC**	158	1394-1413	intron 1
100215	**CC**AGACACCCTATCTT**CTTC**	"	"	intron 1
100244	**CCAG**ACACCCTATCTTCT**TC**	"	"	intron 1

100264	**CCAG**ACACCCTATCTT**CTTC**	"	"	intron 1
100196	**CA**GACACCCTATCTTCTT**CT**	159	1393-1412	intron 1
100216	**CA**GACACCCTATCTTC**TTCT**	"	"	intron 1
100245	**CAGA**CACCCTATCTTCTT**CT**	"	"	intron 1
100265	**CAGA**CACCCTATCTTC**TTCT**	"	"	intron 1
100197	**AG**ACACCCTATCTTCTTC**TC**	160	1392-1411	intron 1
100217	**AG**ACACCCTATCTTCT**TCTC**	"	"	intron 1
100246	**AGAC**ACCCTATCTTCTTC**TC**	"	"	intron 1
100266	**AGAC**ACCCTATCTTCT**TCTC**	"	"	intron 1
100198	**GA**CACCCTATCTTCTTCT**CT**	161	1391-1410	intron 1
100218	**GA**CACCCTATCTTCTT**CTCT**	"	"	intron 1
100247	**GACA**CCCTATCTTCTTCT**CT**	"	"	intron 1
100267	**GACA**CCCTATCTTCTT**CTCT**	"	"	intron 1
100199	**AC**ACCCTATCTTCTTCTC**TC**	162	1390-1409	intron 1
100219	**AC**ACCCTATCTTCTTC**TCTC**	"	"	intron 1
100248	**ACAC**CCTATCTTCTTCTC**TC**	"	"	intron 1
100268	**ACAC**CCTATCTTCTTC**TCTC**	"	"	intron 1
100200	**CA**CCCTATCTTCTTCTCT**CC**	163	1389-1408	intron 1
100220	**CA**CCCTATCTTCTTCT**CTCC**	"	"	intron 1
100249	**CACC**CTATCTTCTTCTCT**CC**	"	"	intron 1
100269	**CACC**CTATCTTCTTCT**CTCC**	"	"	intron 1
100270	**GTC**TTCTGTGTGCCA**GAC**	164	1408-1425	intron 1
100271	**TCT**TCTGTGTGCCAG**ACA**	165	1407-1424	intron 1
100272	**CTT**CTGTGTGCCAGA**CAC**	166	1406-1423	intron 1
100273	**TTC**TGTGTGCCAGAC**ACC**	167	1405-1422	intron 1
100274	**TCT**GTGTGCCAGACA**CCC**	168	1404-1421	intron 1
100275	**CTG**TGTGCCAGACAC**CCT**	169	1403-1420	intron 1
100276	**TGT**GTGCCAGACACC**CTA**	170	1402-1419	intron 1
100277	**GTG**TGCCAGACACCC**TAT**	171	1401-1418	intron 1
100278	**TGT**GCCAGACACCCT**ATC**	172	1400-1417	intron 1
100279	**TGC**CAGACACCCTAT**CTT**	173	1398-1415	intron 1
100280	**GCC**AGACACCCTATC**TTC**	174	1397-1414	intron 1
100281	**CCA**GACACCCTATCT**TCT**	175	1396-1413	intron 1

100282	**CAG**ACACCCTATCTT**CTT**	176	1395-1412	intron 1
100283	**AGA**CACCCTATCTTC**TTC**	177	1394-1411	intron 1
100284	**GAC**ACCCTATCTTCT**TCT**	178	1393-1410	intron 1
100285	**ACA**CCCTATCTTCTT**CTC**	179	1392-1409	intron 1

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethyl cytosines and 2'-deoxy cytosines residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2]Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

EXAMPLE 22: Design of Antisense Oligonucleotides Targeting Human TNF-α Intron 2

Additional antisense oligonucleotides targeted to intron 2 and coding regions of human TNF-α were designed. These are shown in Table 32. Oligonucleotides are screened by RT-PCR as described in Example 5 hereinabove.

TABLE 32

Nucleotide Sequences of Human TNF-α Intron 2 Antisense Oligonucleotides

ISIS No.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
100549	AGAGGTTTGGAGACACTTAC	180	1635-1654	intron 2
100566	**AG**AGGTTTGGAGACACTT**AC**	"	"	intron 2
100550	GAATTAGGAAAGAGGTTTGG	181	1645-1664	intron 2
100567	**GA**ATTAGGAAAGAGGTTT**GG**	"	"	intron 2
100551	CCCAAACCCAGAATTAGGAA	182	1655-1674	intron 2
100568	**CC**CAAACCCAGAATTAGG**AA**	"	"	intron 2
100552	TACCCCCAAACCCAAACCCA	183	1665-1684	intron 2
100569	**TA**CCCCCAAACCCAAACC**CA**	"	"	intron 2
100553	GTACTAACCCTACCCCCAAA	184	1675-1694	intron 2
100570	**GT**ACTAACCCTACCCCCA**AA**	"	"	intron 2

100554	TTCCATACCGGTACTAACCC	185	1685-1704	intron 2
100571	**TT**CCATACCGGTACTAAC**CC**	"	"	intron 2
100555	CCCCCACTGCTTCCATACCG	186	1695-1714	intron 2
100572	**CC**CCCACTGCTTCCATAC**CG**	"	"	intron 2
100556	CTTTAAATTTCCCCCACTGC	187	1705-1724	intron 2
100573	**CT**TTAAATTTCCCCCACT**GC**	"	"	intron 2
100557	AAGACCAAAACTTTAAATTT	188	1715-1734	intron 2
100571	**AA**GACCAAAACTTTAAAT**TT**	"	"	intron 2
100558	ATCCTCCCCCAAGACCAAAA	189	1725-1744	intron 2
100640	**AT**CCTCCCCCAAGACCAA**AA**	"	"	intron 2
100559	ACCTCCATCCATCCTCCCCC	190	1735-1754	intron 2
100641	**AC**CTCCATCCATCCTCCC**CC**	"	"	intron 2
100560	CCCTACTTTCACCTCCATCC	191	1745-1764	intron 2
100642	**CC**CTACTTTCACCTCCAT**CC**	"	"	intron 2
100561	GAAAATACCCCCCTACTTTC	192	1755-1774	intron 2
100643	**GA**AAATACCCCCCTACTT**TC**	"	"	intron 2
100562	AAACTTCCTAGAAAATACCC	193	1765-1784	intron 2
100644	**AA**ACTTCCTAGAAAATAC**CC**	"	"	intron 2
100563	TGAGACCCTTAAACTTCCTA	194	1775-1794	intron 2
100645	**TG**AGACCCTTAAACTTCC**TA**	"	"	intron 2
100564	AAGAAAAAGCTGAGACCCTT	195	1785-1804	intron 2
100646	**AA**GAAAAAGCTGAGACCC**TT**	"	"	intron 2
100565	GGAGAGAGAAAAGAAAAAGC	196	1795-1814	intron 2
100647	**GG**AGAGAGAAAAGAAAAA**GC**	"	"	intron 2
100575	**TGAGCCAGAAGAGGTTGAGG**	197	2665-2684	coding
100576	**ATTCTCTTTTTGAGCCAGAA**	198	2675-2694	coding
100577	**TAAGCCCCCAATTCTCTTTT**	199	2685-2704	coding
100578	**GTTCCGACCCTAAGCCCCCA**	200	2695-2714	coding
100579	**CTAAGCTTGGGTTCCGACCC**	201	2705-2724	coding
100580	**GCTTAAAGTTCTAAGCTTGG**	202	2715-2734	coding
100581	**TGGTCTTGTTGCTTAAAGTT**	203	2725-2744	coding
100582	**TTCGAAGTGGTGGTCTTGTT**	204	2735-2754	coding
100583	**AATCCCAGGTTTCGAAGTGG**	205	2745-2764	coding

100584	CACATTCCTGAATCCCAGGT	206	2755-2774	coding
100585	GTGCAGGCCACACATTCCTG	207	2765-2784	coding
100586	GCACTTCACTGTGCAGGCCA	208	2775-2794	coding
100587	GTGGTTGCCAGCACTTCACT	209	2785-2804	coding
100588	TGAATTCTTAGTGGTTGCCA	210	2795-2814	coding
100589	GGCCCCAGTTTGAATTCTTA	211	2805-2824	coding
100590	GAGTTCTGGAGGCCCCAGTT	212	2815-2834	coding
100591	AGGCCCCAGTGAGTTCTGGA	32	2825-2844	coding
100592	TCAAAGCTGTAGGCCCCAGT	214	2835-2854	coding
100593	ATGTCAGGGATCAAAGCTGT	215	2845-2864	coding
100594	CAGATTCCAGATGTCAGGGA	216	2855-2874	coding
100595	CCCTGGTCTCCAGATTCCAG	217	2865-2884	coding
100596	ACCAAAGGCTCCCTGGTCTC	218	2875-2894	coding
100597	TCTGGCCAGAACCAAAGGCT	219	2885-2904	coding
100598	CCTGCAGCATTCTGGCCAGA	220	2895-2914	coding
100599	CTTCTCAAGTCCTGCAGCAT	221	2905-2924	coding
100600	TAGGTGAGGTCTTCTCAAGT	222	2915-2934	coding
100601	TGTCAATTTCTAGGTGAGGT	223	2925-2944	coding
100602	GGTCCACTTGTGTCAATTTC	224	2935-2954	coding
100603	GAAGGCCTAAGGTCCACTTG	225	2945-2964	coding
100604	CTGGAGAGAGGAAGGCCTAA	226	2955-2974	coding
100605	CTGGAAACATCTGGAGAGAG	227	2965-2984	coding
100606	TCAAGGAAGTCTGGAAACAT	228	2975-2994	coding
100607	GCTCCGTGTCTCAAGGAAGT	229	2985-3004	coding
100608	ATAAATACATTCATCTGTAA	230	3085-3104	coding
100609	GGTCTCCCAAATAAATACAT	231	3095-3114	coding
100610	AGGATACCCCGGTCTCCCAA	232	3105-3124	coding
100611	TGGGTCCCCCAGGATACCCC	35	3115-3134	coding
100612	GCTCCTACATTGGGTCCCCC	234	3125-3144	coding
100613	AGCCAAGGCAGCTCCTACAT	235	3135-3154	coding
100614	AACATGTCTGAGCCAAGGCA	236	3145-3164	coding
100615	TTTCACGGAAAACATGTCTG	237	3155-3174	coding
100616	TCAGCTCCGTTTTCACGGAA	238	3165-3184	coding

100617	**AGCCTATTGTTCAGCTCCGT**	239	3175-3194	coding
100618	**ACATGGGAACAGCCTATTGT**	240	3185-3204	coding
100619	**ATCAAAAGAAGGCACAGAGG**	241	3215-3234	coding
100620	**GTTTAGACAACTTAATCAGA**	242	3255-3274	coding
100621	**AATCAGCATTGTTTAGACAA**	243	3265-3284	coding
100622	**TTGGTCACCAAATCAGCATT**	244	3275-3294	coding
100623	**TGAGTGACAGTTGGTCACCA**	245	3285-3304	coding
100624	**GGCTCAGCAATGAGTGACAG**	246	3295-3314	coding
100625	**ATTACAGACACAACTCCCCT**	247	3325-3344	coding
100626	**TAGTAGGGCGATTACAGACA**	248	3335-3354	coding
100627	**CGCCACTGAATAGTAGGGCG**	249	3345-3364	coding
100628	**CTTTATTTCTCGCCACTGAA**	250	3355-3374	coding

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethyl cytosines and 2'-deoxy cytosines residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

Several of these oligonucleotides were chosen for dose response studies. Cells were grown and treated as described in Example 3. Results are shown in Table 33. Each oligonucleotide tested showed a dose response curve with maximum inhibition greater than 75%.

TABLE 33

Dose Response of PMA-Induced neoHK Cells to TNF-α Antisense Oligonucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
100235	149	intron 1	75 nM	77%	23%
"	"	"	150 nM	25%	75%
"	"	"	300 nM	6%	94%

100243	157	intron 1	75 nM	68%	32%
"	"	"	150 nM	15%	85%
"	"	"	300 nM	6%	94%
100263	157	intron 1	75 nM	79%	21%
"	"	"	150 nM	30%	70%
"	"	"	300 nM	23%	77%

EXAMPLE 23: Optimization of Human TNF-α Antisense Oligonucleotide Chemistry

Analogs of oligonucleotides 21820 (SEQ ID NO. 66) and 21823 (SEQ ID NO. 69) were designed and synthesized to find an optimum gap size. The sequences and chemistries are shown in Table 34.

Dose response experiments were performed as described in Example 3. Results are shown in Table 35.

TABLE 34

Nucleotide Sequences of TNF-α Chimeric Backbone (deoxy gapped) Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
21820	ATATTTCCCGCTCTTTCTGT	66	1339-1358	intron 1
28086	**AT**ATTTCCCGCTCTTTCT**GT**	"	"	"
28087	**ATAT**TTCCCGCTCTTT**CTGT**	"	"	"
21823	GTGTGCCAGACACCCTATCT	69	1399-1418	intron 1
28088	**GT**GTGCCAGACACCCTAT**CT**	"	"	"
28089	**GTGT**GCCAGACACCCT**ATCT**	"	"	"

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines and 2'-deoxycytidines are 5-methyl-cytidines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

TABLE 35

Dose Response of 20 Hour PMA-Induced neoHK Cells to TNF-α Chimeric (deoxy gapped) Antisense Oligonucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% protein Expression	% protein Inhibition
induced	---	---	---	100%	---
13393	49	control	75 nM	150.0%	---
"	"	"	150 nM	135.0%	---
"	"	"	300 nM	90.0%	10.0%
21820	66	intron 1	75 nM	65.0%	35.0%
"	"	"	150 nM	28.0%	72.0%
"	"	"	300 nM	9.7%	90.3%
28086	66	intron 1	75 nM	110.0%	---
"	"	"	150 nM	83.0%	17.0%
"	"	"	300 nM	61.0%	39.0%
28087	66	intron 1	75 nM	127.0%	---
"	"	"	150 nM	143.0%	---
"	"	"	300 nM	147.0%	---
21823	69	intron 1	75 nM	35.0%	65.0%
"	"	"	150 nM	30.0%	70.0%
"	"	"	300 nM	6.4%	93.6%
28088	69	intron 1	75 nM	56.0%	44.0%
"	"	"	150 nM	26.0%	74.0%
"	"	"	300 nM	11.0%	89.0%
28089	69	intron 1	75 nM	76.0%	24.0%
"	"	"	150 nM	53.0%	47.0%
"	"	"	300 nM	23.0%	77.0%

EXAMPLE 24: Screening of additional TNF-α chimeric (deoxy gapped) antisense oligonucleotides

Additional oligonucleotides targeting the major regions of TNF-α were synthesized. Oligonucleotides were synthesized as uniformly phosphorothioate chimeric oligonucleotides having regions of five 2'-O-methoxyethyl (2'-MOE) nucleotides at the wings and a central region of ten deoxynucleotides. Oligonucleotide sequences are shown in Table 36.

Oligonucleotides were screened as described in Example 5. Results are shown in Table 37.

TABLE 36

Nucleotide Sequence of Additional Human TNF-α Chimeric (deoxy gapped) Antisense Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
104649	**CTGAG**GGAGCGTCTG**CTGGC**	251	0616-0635	5'-UTR
104650	**CCTTG**CTGAGGGAGC**GTCTG**	252	0621-0640	5'-UTR
104651	**CTGGT**CCTCTGCTGT**CCTTG**	253	0636-0655	5'-UTR
104652	**CCTCT**GCTGTCCTTG**CTGAG**	254	0631-0650	5'-UTR
104653	**TTCTC**TCCCTCTTAG**CTGGT**	255	0651-0670	5'-UTR
104654	**TCCCT**CTTAGCTGGT**CCTCT**	256	0646-0665	5'-UTR
104655	**TCTGA**GGGTTGTTTT**CAGGG**	257	0686-0705	5'-UTR
104656	**CTGTA**GTTGCTTCTC**TCCCT**	258	0661-0680	5'-UTR
104657	**ACCTG**CCTGGCAGCT**TGTCA**	259	0718-0737	5'-UTR
104658	**GGATG**TGGCGTCTGA**GGGTT**	260	0696-0715	5'-UTR
104659	**TGTGA**GAGGAAGAGA**ACCTG**	261	0733-0752	5'-UTR
104660	**GAGGA**AGAGAACCTG**CCTGG**	262	0728-0747	5'-UTR
104661	**AGCCG**TGGGTCAGTA**TGTGA**	263	0748-0767	5'-UTR
104662	**TGGGT**CAGTATGTGA**GAGGA**	264	0743-0762	5'-UTR
104663	**GAGAG**GGTGAAGCCG**TGGGT**	265	0758-0777	5'-UTR

104664	**TCATG**GTGTCCTTTC**CAGGG**	266	0780-0799	AUG
104665	**CTTTC**AGTGCTCATG**GTGTC**	267	0790-0809	AUG
104666	**TCATG**CTTTCAGTGC**TCATG**	268	0795-0814	AUG
104667	**ACGTC**CCGGATCATG**CTTTC**	269	0805-0824	coding
104668	**GCTCC**ACGTCCCGGA**TCATG**	270	0810-0829	coding
104669	**TCCTC**GGCCAGCTCC**ACGTC**	271	0820-0839	coding
104670	**GCGCC**TCCTCGGCCA**GCTCC**	272	0825-0844	coding
104671	**AGGAA**CAAGCACCGC**CTGGA**	273	0874-0893	coding
104672	**CAAGC**ACCGCCTGGA**GCCCT**	274	0869-0888	coding
104673	**AAGGA**GAAGAGGCTG**AGGAA**	275	0889-0908	coding
104674	**GAAGA**GGCTGAGGAA**CAAGC**	276	0884-0903	coding
104675	**CCTGC**CACGATCAGG**AAGGA**	277	0904-0923	coding
104676	**CACGA**TCAGGAAGGA**GAAGA**	278	0899-0918	coding
104677	**AAGAG**CGTGGTGGCG**CCTGC**	279	0919-0938	coding
104678	**CGTGG**TGGCGCCTGC**CACGA**	280	0914-0933	coding
104679	**AAGTG**CAGCAGGCAG**AAGAG**	281	0934-0953	coding
104680	**CAGCA**GGCAGAAGAG**CGTGG**	282	0929-0948	coding
104681	**GATCA**CTCCAAAGTG**CAGCA**	283	0944-0963	coding
104682	**GGGCC**GATCACTCCA**AAGTG**	284	0949-0968	coding
104683	**GGGCC**AGAGGGCTGA**TTAGA**	285	1606-1625	coding
104684	**AGAGG**GCTGATTAGA**GAGAG**	286	1601-1620	coding
104685	**GCTAC**AGGCTTGTCA**CTCGG**	287	1839-1858	coding
104686	**CTGAC**TGCCTGGGCC**AGAGG**	288	1616-1635	E2/I2[3]
104687	**TACAA**CATGGGCTAC**AGGCT**	289	1849-1868	coding
104688	**AGCCA**CTGGAGCTGC**CCCTC**	290	2185-2204	coding
104689	**CTGGA**GCTGCCCCTC**AGCTT**	291	2180-2199	coding
104690	**TTGGC**CCGGCGGTTC**AGCCA**	292	2200-2219	coding
104691	**TTGGC**CAGGAGGGCA**TTGGC**	293	2215-2234	coding
104692	**CCGGC**GGTTCAGCCA**CTGGA**	294	2195-2214	coding
104693	**CTCAG**CTCCACGCCA**TTGGC**	295	2230-2249	coding
104694	**CAGGA**GGGCATTGGC**CCGGC**	296	2210-2229	coding
104695	**CTCCA**CGCCATTGGC**CAGGA**	297	2225-2244	coding
104696	**ACCAG**CTGGTTATCT**CTCAG**	298	2245-2264	coding

104697	**CTGGT**TATCTCTCAG**CTCCA**	299	2240-2259	coding
104698	**CCCTC**TGATGGCACC**ACCAG**	300	2260-2279	coding
104699	**TGATG**GCACCACCAG**CTGGT**	301	2255-2274	coding
104700	**TAGAT**GAGGTACAGG**CCCTC**	302	2275-2294	coding
104701	**AAGAG**GACCTGGGAG**TAGAT**	303	2290-2309	coding
104702	**GAGGT**ACAGGCCCTC**TGATG**	304	2270-2289	coding
104703	**CAGCC**TTGGCCCTTG**AAGAG**	305	2305-2324	coding
104704	**GACCT**GGGAGTAGAT**GAGGT**	306	2285-2304	coding
104705	**TTGGC**CCTTGAAGAG**GACCT**	307	2300-2319	coding
104706	**TGGTG**TGGGTGAGGA**GCACA**	308	2337-2356	coding
104707	**CGGCG**ATGCGGCTGA**TGGTG**	309	2352-2371	coding
104708	**TGGGT**GAGGAGCACA**TGGGT**	310	2332-2351	coding
104709	**TGGTC**TGGTAGGAGA**CGGCG**	311	2367-2386	coding
104710	**ATGCG**GCTGATGGTG**TGGGT**	312	2347-2366	coding
104711	**AGAGG**AGGTTGACCT**TGGTC**	313	2382-2401	coding
104712	**TGGTA**GGAGACGGCG**ATGCG**	314	2362-2381	coding
104713	**AGGTT**GACCTTGGTC**TGGTA**	315	2377-2396	coding
104714	**GGCTC**TTGATGGCAG**AGAGG**	316	2397-2416	coding
104715	**TCATA**CCAGGGCTTG**GCCTC**	317	2446-2465	coding
104716	**TTGAT**GGCAGAGAGG**AGGTT**	318	2392-2411	coding
104717	**CCCAG**ATAGATGGGC**TCATA**	93	2461-2480	coding
104718	**CCAGG**GCTTGGCCTC**AGCCC**	94	2441-2460	coding
104719	**AGCTG**GAAGACCCCT**CCCAG**	319	2476-2495	coding
104720	**ATAGA**TGGGCTCATA**CCAGG**	320	2456-2475	coding
104721	**CGGTC**ACCCTTCTCC**AGCTG**	321	2491-2510	coding
104722	**GAAGA**CCCCTCCCAG**ATAGA**	322	2471-2490	coding
104723	**ATCTC**AGCGCTGAGT**CGGTC**	26	2506-2525	coding
104724	**ACCCT**TCTCCAGCTG**GAAGA**	323	2486-2505	coding
104725	**TAGTC**GGGCCGATTG**ATCTC**	90	2521-2540	coding
104726	**AGCGC**TGAGTCGGTC**ACCCT**	91	2501-2520	coding
104727	**TCGGC**AAAGTCGAGA**TAGTC**	324	2536-2554	coding
104728	**GGGCC**GATTGATCTC**AGCGC**	325	2516-2535	coding
104729	**TAGAC**CTGCCCAGAC**TCGGC**	326	2551-2570	coding

104730	**AAAGT**CGAGATAGTC**GGGCC**	327	2531-2550	coding
104731	**GCAAT**GATCCCAAAG**TAGAC**	328	2566-2585	coding
104732	**CTGCC**CAGACTCGGC**AAAGT**	329	2546-2565	coding
104733	**CGTCC**TCCTCACAGG**GCAAT**	330	2581-2600	stop
104734	**GATCC**CAAAGTAGAC**CTGCC**	88	2561-2580	coding
104735	**GGAAG**GTTGGATGTT**CGTCC**	331	2596-2615	3'-UTR
104736	**TCCTC**ACAGGGCAAT**GATCC**	332	2576-2595	stop
104737	**GTTGA**GGGTGTCTGA**AGGAG**	333	2652-2671	3'-UTR
104738	**GTTGG**ATGTTCGTCC**TCCTC**	334	2591-2610	stop
104739	**TTTGA**GCCAGAAGAG**GTTGA**	335	2667-2686	3'-UTR
104740	**GAGGC**GTTTGGGAAG**GTTGG**	336	2606-2625	3'-UTR
104741	**GCCCC**CAATTCTCTT**TTTGA**	337	2682-2701	3'-UTR
104742	**GCCAG**AAGAGGTTGA**GGGTG**	338	2662-2681	3'-UTR
104743	**GGGTT**CCGACCCTAA**GCCCC**	339	2697-2716	3'-UTR
104744	**CAATT**CTCTTTTTGA**GCCAG**	340	2677-2696	3'-UTR
104745	**TAAAG**TTCTAAGCTT**GGGTT**	341	2712-2731	3'-UTR
104746	**CCGAC**CCTAAGCCCC**CAATT**	342	2692-2711	3'-UTR
104747	**GGTGG**TCTTGTTGCT**TAAAG**	343	2727-2746	3'-UTR
104748	**TTCTA**AGCTTGGGTT**CCGAC**	344	2707-2726	3'-UTR
104749	**CCCAG**GTTTCGAAGT**GGTGG**	345	2742-2761	3'-UTR
104750	**TCTTG**TTGCTTAAAG**TTCTA**	346	2722-2741	3'-UTR
104751	**CACAC**ATTCCTGAAT**CCCAG**	347	2757-2776	3'-UTR
104752	**GTTTC**GAAGTGGTGG**TCTTG**	348	2737-2756	3'-UTR
104753	**CTTCA**CTGTGCAGGC**CACAC**	349	2772-2791	3'-UTR
104754	**ATTCC**TGAATCCCAG**GTTTC**	350	2752-2771	3'-UTR
104755	**TAGTG**GTTGCCAGCA**CTTCA**	351	2787-2806	3'-UTR
104756	**CCCAG**TTTGAATTCT**TAGTG**	352	2802-2821	3'-UTR
104757	**CTGTG**CAGGCCACAC**ATTCC**	353	2767-2786	3'-UTR
104758	**GTGAG**TTCTGGAGGC**CCCAG**	354	2817-2836	3'-UTR
104759	**GTTGC**CAGCACTTCA**CTGTG**	355	2782-2801	3'-UTR
104760	**TTTGA**ATTCTTAGTG**GTTGC**	356	2797-2816	3'-UTR
104761	**AAGCT**GTAGGCCCCA**GTGAG**	357	2832-2851	3'-UTR
104762	**TTCTG**GAGGCCCCAG**TTTGA**	358	2812-2831	3'-UTR

104763	**AGATG**TCAGGGATCA**AAGCT**	359	2847-2866	3'-UTR
104764	**TGGTC**TCCAGATTCC**AGATG**	360	2862-2881	3'-UTR
104765	**GTAGG**CCCCAGTGAG**TTCTG**	361	2827-2846	3'-UTR
104766	**GAACC**AAAGGCTCCC**TGGTC**	362	2877-2896	3'-UTR
104767	**TCAGG**GATCAAAGCT**GTAGG**	363	2842-2861	3'-UTR
104768	**TCCAG**ATTCCAGATG**TCAGG**	364	2857-2876	3'-UTR
104769	**GCAGC**ATTCTGGCCA**GAACC**	365	2892-2911	3'-UTR
104770	**GTCTT**CTCAAGTCCT**GCAGC**	366	2907-2926	3'-UTR
104771	**AAAGG**CTCCCTGGTC**TCCAG**	367	2872-2891	3'-UTR
104772	**CAATT**TCTAGGTGAG**GTCTT**	368	2922-2941	3'-UTR
104773	**ATTCT**GGCCAGAACC**AAAGG**	369	2887-2906	3'-UTR
104774	**CTCAA**GTCCTGCAGC**ATTCT**	34	2902-2921	3'-UTR
104775	**AAGGT**CCACTTGTGT**CAATT**	370	2937-2956	3'-UTR
104776	**GAGAG**AGGAAGGCCT**AAGGT**	371	2952-2971	3'-UTR
104777	**TCTAG**GTGAGGTCTT**CTCAA**	372	2917-2936	3'-UTR
104778	**CCACT**TGTGTCAATT**TCTAG**	373	2932-2951	3'-UTR
104779	**GTCTG**GAAACATCTG**GAGAG**	374	2967-2986	3'-UTR
104780	**CCGTG**TCTCAAGGAA**GTCTG**	375	2982-3001	3'-UTR
104781	**AGGAA**GGCCTAAGGT**CCACT**	376	2947-2966	3'-UTR
104782	**GAGGG**AGCTGGCTCC**ATGGG**	377	3014-3033	3'-UTR
104783	**GAAAC**ATCTGGAGAG**AGGAA**	378	2962-2981	3'-UTR
104784	**GTGCA**AACATAAATA**GAGGG**	379	3029-3048	3'-UTR
104785	**TCTCA**AGGAAGTCTG**GAAAC**	380	2977-2996	3'-UTR
104786	**AATAA**ATAATCACAA**GTGCA**	381	3044-3063	3'-UTR
104787	**GGGCT**GGGCTCCGTG**TCTCA**	382	2992-3011	3'-UTR
104788	**TACCC**CGGTCTCCCA**AATAA**	383	3101-3120	3'-UTR
104789	**AACAT**AAATAGAGGG**AGCTG**	384	3024-3043	3'-UTR
104790	**TTGGG**TCCCCCAGGA**TACCC**	385	3116-3135	3'-UTR
104791	**ATAAT**CACAAGTGCA**AACAT**	386	3039-3058	3'-UTR
104792	**AAGGC**AGCTCCTACA**TTGGG**	387	3131-3150	3'-UTR
104793	**CGGTC**TCCCAAATAA**ATACA**	388	3096-3115	3'-UTR
104794	**AAACA**TGTCTGAGCC**AAGGC**	389	3146-3165	3'-UTR
104795	**TCCCC**CAGGATACCC**CGGTC**	390	3111-3130	3'-UTR

104796	**AGCTC**CTACATTGGG**TCCCC**	391	3126-3145	3'-UTR
104797	**CTCCG**TTTTCACGGA**AAACA**	37	3161-3180	3'-UTR
104798	**TGTCT**GAGCCAAGGC**AGCTC**	392	3141-3160	3'-UTR
104799	**CAGCC**TATTGTTCAG**CTCCG**	393	3176-3195	3'-UTR
104800	**AGAAG**GCACAGAGGC**CAGGG**	394	3209-3228	3'-UTR
104801	**TTTTC**ACGGAAAACA**TGTCT**	395	3156-3175	3'-UTR
104802	**TATTG**TTCAGCTCCG**TTTTC**	396	3171-3190	3'-UTR
104803	**AAAAA**CATAATCAAA**AGAAG**	397	3224-3243	3'-UTR
104804	**CAGAT**AAATATTTTA**AAAAA**	398	3239-3258	3'-UTR
104805	**TACAT**GGGAACAGCC**TATTG**	399	3186-3205	3'-UTR
104806	**TTTAG**ACAACTTAAT**CAGAT**	400	3254-3273	3'-UTR
104807	**CATAA**TCAAAAGAAG**GCACA**	401	3219-3238	3'-UTR
104808	**ACCAA**ATCAGCATTG**TTTAG**	402	3269-3288	3'-UTR
104809	**AAATA**TTTTAAAAAA**CATAA**	403	3234-3253	3'-UTR
104810	**GAGTG**ACAGTTGGTC**ACCAA**	404	3284-3303	3'-UTR
104811	**ACAAC**TTAATCAGAT**AAATA**	405	3249-3268	3'-UTR
104812	**CAGAG**GCTCAGCAAT**GAGTG**	406	3299-3318	3'-UTR
104813	**ATCAG**CATTGTTTAG**ACAAC**	407	3264-3283	3'-UTR
104814	**AGGGC**GATTACAGAC**ACAAC**	408	3331-3350	3'-UTR
104815	**ACAGT**TGGTCACCAA**ATCAG**	409	3279-3298	3'-UTR
104816	**TCGCC**ACTGAATAGT**AGGGC**	410	3346-3365	3'-UTR
104817	**GCTCA**GCAATGAGTG**ACAGT**	411	3294-3313	3'-UTR
104818	**AGCAA**ACTTTATTTC**TCGCC**	412	3361-3380	3'-UTR
104819	**GATTA**CAGACACAAC**TCCCC**	413	3326-3345	3'-UTR
104820	**ACTGA**ATAGTAGGGC**GATTA**	414	3341-3360	3'-UTR
104821	**ACTTT**ATTTCTCGCC**ACTGA**	415	3356-3375	3'-UTR
104822	**GCTGT**CCTTGCTGAG**GGAGC**	416	0626-0645	5'-UTR
104823	**CTTAG**CTGGTCCTCT**GCTGT**	417	0641-0660	5'-UTR
104824	**GTTGC**TTCTCTCCCT**CTTAG**	418	0656-0675	5'-UTR
104825	**TGGCG**TCTGAGGGTT**GTTTT**	419	0691-0710	5'-UTR
104826	**AGAGA**ACCTGCCTGG**CAGCT**	420	0723-0742	5'-UTR
104827	**CAGTA**TGTGAGAGGA**AGAGA**	421	0738-0757	5'-UTR
104828	**GGTGA**AGCCGTGGGT**CAGTA**	422	0753-0772	5'-UTR

104829	**AGTGC**TCATGGTGTC**CTTTC**	423	0785-0804	AUG
104830	**CCGGA**TCATGCTTTC**AGTGC**	424	0800-0819	coding
104831	**GGCCA**GCTCCACGTC**CCGGA**	425	0815-0834	coding
104832	**GGCCC**CCCTGTCTTC**TTGGG**	426	0847-0866	coding
104833	**GGCTG**AGGAACAAGC**ACCGC**	427	0879-0898	coding
104834	**TCAGG**AAGGAGAAGA**GGCTG**	428	0894-0913	coding
104835	**TGGCG**CCTGCCACGA**TCAGG**	429	0909-0918	coding
104836	**GGCAG**AAGAGCGTGG**TGGCG**	430	0924-0943	coding
104837	**CTCCA**AAGTGCAGCA**GGCAG**	431	0939-0958	coding
104838	**GCTGA**TTAGAGAGAG**GTCCC**	432	1596-1615	coding
104839	**TGCCT**GGGCCAGAGG**GCTGA**	433	1611-1630	coding
104840	**GCTGC**CCCTCAGCTT**GAGGG**	434	2175-2194	coding
104841	**GGTTC**AGCCACTGGA**GCTGC**	435	2190-2209	coding
104842	**GGGCA**TTGGCCCGGC**GGTTC**	436	2205-2224	coding
104843	**CGCCA**TTGGCCAGGA**GGGCA**	437	2220-2239	coding
104844	**TATCT**CTCAGCTCCA**CGCCA**	438	2235-2254	coding
104845	**GCACC**ACCAGCTGGT**TATCT**	439	2250-2269	coding
104846	**ACAGG**CCCTCTGATG**GCACC**	440	2265-2284	coding
104847	**GGGAG**TAGATGAGGT**ACAGG**	441	2280-2299	coding
104848	**CCTTG**AAGAGGACCT**GGGAG**	442	2295-2314	coding
104849	**GAGGA**GCACATGGGT**GGAGG**	443	2327-2346	coding
104850	**GCTGA**TGGTGTGGGT**GAGGA**	444	2342-2361	coding
104851	**GGAGA**CGGCGATGCG**GCTGA**	445	2357-2376	coding
104852	**GACCT**TGGTCTGGTA**GGAGA**	446	2372-2391	coding
104853	**GGCAG**AGAGGAGGTT**GACCT**	447	2387-2406	coding
104854	**GCTTG**GCCTCAGCCC**CCTCT**	23	2436-2455	coding
104855	**TGGGC**TCATACCAGG**GCTTG**	448	2451-2470	coding
104856	**CCCCT**CCCAGATAGA**TGGGC**	449	2466-2485	coding
104857	**TCTCC**AGCTGGAAGA**CCCCT**	92	2481-2500	coding
104858	**TGAGT**CGGTCACCCT**TCTCC**	450	2496-2515	coding
104859	**GATTG**ATCTCAGCGC**TGAGT**	451	2511-2530	coding
104860	**CGAGA**TAGTCGGGCC**GATTG**	452	2526-2545	coding

104861	**CAGAC**TCGGCAAAGT**CGAGA**	89	2541-2560	coding
104862	**CAAAG**TAGACCTGCC**CAGAC**	453	2556-2575	coding
104863	**ACAGG**GCAATGATCC**CAAAG**	454	2571-2590	stop
104864	**ATGTT**CGTCCTCCTC**ACAGG**	455	2586-2605	stop
104865	**GTTTG**GGAAGGTTGG**ATGTT**	456	2601-2620	3'-UTR
104866	**AAGAG**GTTGAGGGTG**TCTGA**	457	2657-2676	3'-UTR
104867	**CTCTT**TTTGAGCCAG**AAGAG**	458	2672-2691	3'-UTR
104868	**CCTAA**GCCCCCAATT**CTCTT**	459	2687-2706	3'-UTR
104869	**AGCTT**GGGTTCCGAC**CCTAA**	460	2702-2721	3'-UTR
104870	**TTGCT**TAAAGTTCTA**AGCTT**	461	2717-2736	3'-UTR
104871	**GAAGT**GGTGGTCTTG**TTGCT**	462	2732-2751	3'-UTR
104872	**TGAAT**CCCAGGTTTC**GAAGT**	463	2747-2766	3'-UTR
104873	**CAGGC**CACACATTCC**TGAAT**	464	2762-2781	3'-UTR
104874	**CAGCA**CTTCACTGTG**CAGGC**	465	2777-2796	3'-UTR
104875	**ATTCT**TAGTGGTTGC**CAGCA**	466	2792-2811	3'-UTR
104876	**GAGGC**CCCAGTTTGA**ATTCT**	467	2807-2826	3'-UTR
104877	**CCCCA**GTGAGTTCTG**GAGGC**	468	2822-2841	3'-UTR
104878	**GATCA**AAGCTGTAGG**CCCCA**	469	2837-2856	3'-UTR
104879	**ATTCC**AGATGTCAGG**GATCA**	470	2852-2871	3'-UTR
104880	**CTCCC**TGGTCTCCAG**ATTCC**	471	2867-2886	3'-UTR
104881	**GGCCA**GAACCAAAGG**CTCCC**	472	2882-2901	3'-UTR
104882	**GTCCT**GCAGCATTCT**GGCCA**	473	2897-2916	3'-UTR
104883	**GTGAG**GTCTTCTCAA**GTCCT**	474	2912-2931	3'-UTR
104884	**TGTGT**CAATTTCTAG**GTGAG**	475	2927-2946	3'-UTR
104885	**GGCCT**AAGGTCCACT**TGTGT**	476	2942-2961	3'-UTR
104886	**ATCTG**GAGAGAGGAA**GGCCT**	477	2957-2976	3'-UTR
104887	**AGGAA**GTCTGGAAAC**ATCTG**	478	2972-2991	3'-UTR
104888	**GGGCT**CCGTGTCTCA**AGGAA**	479	2987-3006	3'-UTR
104889	**AAATA**GAGGGAGCTG**GCTCC**	480	3019-3038	3'-UTR
104890	**CACAA**GTGCAAACAT**AAATA**	481	3034-3053	3'-UTR
104891	**TCCCA**AATAAATACA**TTCAT**	482	3091-3110	3'-UTR
104892	**CAGGA**TACCCCGGTC**TCCCA**	483	3106-3125	3'-UTR
104893	**CTACA**TTGGGTCCCC**CAGGA**	484	3121-3140	3'-UTR

104894	**GAGCC**AAGGCAGCTC**CTACA**	485	3136-3155	3'-UTR
104895	**ACGGA**AAACATGTCT**GAGCC**	486	3151-3170	3'-UTR
104896	**TTCAG**CTCCGTTTTC**ACGGA**	487	3166-3185	3'-UTR
104897	**GGGAA**CAGCCTATTG**TTCAG**	488	3181-3200	3'-UTR
104898	**TCAAA**AGAAGGCACA**GAGGC**	489	3214-3233	3'-UTR
104899	**TTTTA**AAAAACATAA**TCAAA**	490	3229-3248	3'-UTR
104900	**TTAAT**CAGATAAATA**TTTTA**	491	3244-3263	3'-UTR
104901	**CATTG**TTTAGACAAC**TTAAT**	492	3259-3278	3'-UTR
104902	**TGGTC**ACCAAATCAG**CATTG**	493	3274-3293	3'-UTR
104903	**GCAAT**GAGTGACAGT**TGGTC**	494	3289-3308	3'-UTR
104904	**GGGAG**CAGAGGCTCA**GCAAT**	495	3304-3323	3'-UTR
104905	**ATAGT**AGGGCGATTA**CAGAC**	496	3336-3355	3'-UTR
104906	**ATTTC**TCGCCACTGA**ATAGT**	497	3351-3370	3'-UTR

[1] Emboldened residues are 2'-O-methoxyethyl residues (others are 2'-deoxy-). All 2'-O-methoxyethyl cytosines and 2'-deoxy cytosines residues are 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2]Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

[3] This target region is an exon-intron junction and is represented in the form, for example, I1/E2, where I, followed by a number, refers to the intron number and E, followed by a number, refers to the exon number.

TABLE 37

Inhibition of Human TNF-α mRNA Expression by Chimeric (deoxy gapped) Phosphorothioate Oligodeoxynucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
basal	---	---	0.0%	---
induced	---	---	100.0%	0.0%
28089	69	intron 1	42.3%	57.7%
104649	251	5'-UTR	165.6%	---

104650	252	5'-UTR	75.8%	24.2%
104651	253	5'-UTR	58.2%	41.8%
104652	254	5'-UTR	114.5%	---
104653	255	5'-UTR	84.9%	15.1%
104654	256	5'-UTR	80.8%	19.2%
104655	257	5'-UTR	94.3%	5.7%
104656	258	5'-UTR	78.4%	21.6%
104657	259	5'-UTR	87.4%	12.6%
104658	260	5'-UTR	213.4%	---
104659	261	5'-UTR	96.3%	3.7%
104660	262	5'-UTR	153.1%	---
104661	263	5'-UTR	90.0%	10.0%
104662	264	5'-UTR	33.3%	66.7%
104663	265	5'-UTR	144.2%	---
104664	266	AUG	76.3%	23.7%
104665	267	AUG	185.3%	---
104666	268	AUG	67.4%	32.6%
104667	269	Coding	94.3%	5.7%
104668	270	Coding	63.1%	36.9%
104669	271	Coding	50.8%	49.2%
104670	272	Coding	43.7%	56.3%
104671	273	Coding	52.2%	47.8%
104672	274	Coding	51.8%	48.2%
104673	275	Coding	102.3%	---
104674	276	Coding	135.4%	---
104675	277	Coding	83.1%	16.9%
104676	278	Coding	87.5%	12.5%
104677	279	Coding	53.6%	46.4%
104678	280	Coding	75.2%	24.8%
104679	281	Coding	114.0%	---
104680	282	Coding	142.5%	---
104681	283	Coding	58.5%	41.5%
104682	284	Coding	101.9%	---
104683	285	Coding	77.1%	22.9%

104684	286	Coding	61.0%	39.0%
104685	287	Coding	65.9%	34.1%
104686	288	E2/I2	59.2%	40.8%
104687	289	Coding	77.0%	23.0%
104688	290	Coding	40.1%	59.9%
104689	291	Coding	78.6%	21.4%
104690	292	Coding	90.9%	9.1%
104691	293	Coding	107.6%	---
104692	294	Coding	63.4%	36.6%
104693	295	Coding	74.1%	25.9%
104694	296	Coding	108.3%	---
104695	297	Coding	48.2%	51.8%
104696	298	Coding	120.3%	---
104697	299	Coding	45.0%	55.0%
104698	300	Coding	77.1%	22.9%
104699	301	Coding	143.7%	---
104700	302	Coding	96.1%	3.9%
104701	303	Coding	106.8%	---
104702	304	Coding	157.4%	---
104703	305	Coding	84.3%	15.7%
104704	306	Coding	182.8%	---
104705	307	Coding	125.1%	---
104706	308	Coding	81.8%	18.2%
104707	309	Coding	104.8%	---
104708	310	Coding	163.0%	---
104709	311	Coding	95.0%	5.0%
104710	312	Coding	182.1%	---
104711	313	Coding	82.1%	17.9%
104712	314	Coding	118.1%	---
104713	315	Coding	31.1%	68.9%
104714	316	Coding	90.5%	9.5%
104715	317	Coding	96.7%	3.3%
104716	318	Coding	180.7%	---
104717	93	Coding	71.6%	28.4%

104718	94	Coding	187.0%	---
104719	319	Coding	88.8%	11.2%
104720	320	Coding	166.5%	---
104721	321	Coding	65.0%	35.0%
104722	322	Coding	59.6%	40.4%
104723	26	Coding	90.1%	9.9%
104724	323	Coding	88.7%	11.3%
104725	90	Coding	94.7%	5.3%
104726	91	Coding	84.1%	15.9%
104727	324	Coding	125.3%	---
104728	325	Coding	221.7%	---
104729	326	Coding	102.4%	---
104730	327	Coding	151.6%	---
104731	328	Coding	102.2%	---
104732	329	Coding	53.2%	46.8%
104733	330	Stop	57.0%	43.0%
104734	88	Coding	119.2%	---
104735	331	3'-UTR	71.2%	28.8%
104736	332	Stop	79.0%	21.0%
104737	333	3'-UTR	87.4%	12.6%
104738	334	Stop	36.8%	63.2%
104739	335	3'-UTR	106.0%	---
104740	336	3'-UTR	130.9%	---
104741	337	3'-UTR	79.2%	20.8%
104742	338	3'-UTR	159.0%	---
104743	339	3'-UTR	96.1%	3.9%
104744	340	3'-UTR	129.9%	---
104745	341	3'-UTR	80.2%	19.8%
104746	342	3'-UTR	168.8%	---
104747	343	3'-UTR	89.2%	10.8%
104748	344	3'-UTR	103.4%	---
104749	345	3'-UTR	89.0%	11.0%
104750	346	3'-UTR	160.0%	---
104751	347	3'-UTR	60.1%	39.9%

104752	348	3'-UTR	72.4%	27.6%
104753	349	3'-UTR	70.0%	30.0%
104754	350	3'-UTR	115.6%	---
104755	351	3'-UTR	71.7%	28.3%
104756	352	3'-UTR	91.5%	8.5%
104757	353	3'-UTR	85.6%	14.4%
104758	354	3'-UTR	97.6%	2.4%
104759	355	3'-UTR	68.6%	31.4%
104760	356	3'-UTR	182.4%	---
104761	357	3'-UTR	110.9%	---
104762	358	3'-UTR	161.4%	---
104763	359	3'-UTR	102.0%	---
104764	360	3'-UTR	113.5%	---
104765	361	3'-UTR	154.8%	---
104766	362	3'-UTR	126.4%	---
104767	363	3'-UTR	116.1%	---
104768	364	3'-UTR	177.7%	---
104769	365	3'-UTR	89.8%	10.2%
104770	366	3'-UTR	94.3%	5.7%
104771	367	3'-UTR	191.2%	---
104772	368	3'-UTR	80.3%	19.7%
104773	369	3'-UTR	133.9%	---
104774	34	3'-UTR	94.8%	5.2%
104775	370	3'-UTR	80.6%	19.4%
104776	371	3'-UTR	90.1%	9.9%
104777	372	3'-UTR	84.7%	15.3%
104778	373	3'-UTR	121.3%	---
104779	374	3'-UTR	97.8%	2.2%
104780	375	3'-UTR	67.6%	32.4%
104781	376	3'-UTR	141.5%	---
104782	377	3'-UTR	96.5%	3.5%
104783	378	3'-UTR	153.2%	---
104784	379	3'-UTR	85.4%	14.6%
104785	380	3'-UTR	163.9%	---

104786	381	3'-UTR	82.9%	17.1%
104787	382	3'-UTR	89.7%	10.3%
104788	383	3'-UTR	103.9%	---
104789	384	3'-UTR	75.8%	24.2%
104790	385	3'-UTR	106.3%	---
104791	386	3'-UTR	165.3%	---
104792	387	3'-UTR	71.8%	28.2%
104793	388	3'-UTR	101.9%	---
104794	389	3'-UTR	70.7%	29.3%
104795	390	3'-UTR	68.8%	31.2%
104796	391	3'-UTR	93.4%	6.6%
104797	37	3'-UTR	131.7%	---
104798	392	3'-UTR	89.4%	10.6%
104799	393	3'-UTR	89.6%	10.4%
104800	394	3'-UTR	89.0%	11.0%
104801	395	3'-UTR	196.8%	---
104802	396	3'-UTR	189.3%	---
104803	397	3'-UTR	119.7%	---
104804	398	3'-UTR	102.4%	---
104805	399	3'-UTR	90.6%	9.4%
104806	400	3'-UTR	89.1%	10.9%
104807	401	3'-UTR	152.6%	---
104808	402	3'-UTR	96.8%	3.2%
104809	403	3'-UTR	178.8%	---
104810	404	3'-UTR	94.9%	5.1%
104811	405	3'-UTR	234.4%	---
104812	406	3'-UTR	114.3%	---
104813	407	3'-UTR	153.7%	---
104814	408	3'-UTR	86.3%	13.7%
104815	409	3'-UTR	153.9%	---
104816	410	3'-UTR	79.9%	20.1%
104817	411	3'-UTR	196.5%	---
104818	412	3'-UTR	94.3%	5.7%
104819	413	3'-UTR	143.3%	---

104820	414	3'-UTR	123.8%	---
104821	415	3'-UTR	129.2%	---
104822	416	5'-UTR	76.6%	23.4%
104823	417	5'-UTR	63.9%	36.1%
104824	418	5'-UTR	22.0%	78.0%
104825	419	5'-UTR	109.4%	---
104826	420	5'-UTR	45.2%	54.8%
104827	421	5'-UTR	68.9%	31.1%
104828	422	5'-UTR	70.9%	29.1%
104829	423	AUG	46.6%	53.4%
104830	424	Coding	55.0%	45.0%
104831	425	Coding	49.5%	50.5%
104832	426	Coding	106.0%	---
104833	427	Coding	23.7%	76.3%
104834	428	Coding	91.8%	8.2%
104835	429	Coding	72.3%	27.7%
104836	430	Coding	63.4%	36.6%
104837	431	Coding	31.0%	69.0%
104838	432	Coding	18.0%	82.0%
104839	433	Coding	67.9%	32.1%
104840	434	Coding	93.8%	6.2%
104841	435	Coding	43.0%	57.0%
104842	436	Coding	73.2%	26.8%
104843	437	Coding	48.1%	51.9%
104844	438	Coding	39.2%	60.8%
104845	439	Coding	37.6%	62.4%
104846	440	Coding	81.7%	18.3%
104847	441	Coding	50.8%	49.2%
104848	442	Coding	56.7%	43.3%
104849	443	Coding	51.8%	48.2%
104850	444	Coding	91.8%	8.2%
104851	445	Coding	93.9%	6.1%
104852	446	Coding	100.9%	---
104853	447	Coding	67.7%	32.3%

104854	23	Coding	11.0%	89.0%
104855	448	Coding	62.5%	37.5%
104856	449	Coding	67.8%	32.2%
104857	92	Coding	28.1%	71.9%
104858	450	Coding	76.2%	23.8%
104859	451	Coding	52.3%	47.7%
104860	452	Coding	93.6%	6.4%
104861	89	Coding	79.3%	20.7%
104862	453	Coding	63.1%	36.9%
104863	454	Stop	64.5%	35.5%
104864	455	Stop	43.2%	56.8%
104865	456	3'-UTR	83.1%	16.9%
104866	457	3'-UTR	49.4%	50.6%
104867	458	3'-UTR	49.5%	50.5%
104868	459	3'-UTR	89.6%	10.4%
104869	460	3'-UTR	21.4%	78.6%
104870	461	3'-UTR	118.0%	---
104871	462	3'-UTR	55.8%	44.2%
104872	463	3'-UTR	49.0%	51.0%
104873	464	3'-UTR	92.6%	7.4%
104874	465	3'-UTR	33.4%	66.6%
104875	466	3'-UTR	36.2%	63.8%
104876	467	3'-UTR	73.4%	26.6%
104877	468	3'-UTR	40.9%	59.1%
104878	469	3'-UTR	78.7%	21.3%
104879	470	3'-UTR	75.4%	24.6%
104880	471	3'-UTR	50.2%	49.8%
104881	472	3'-UTR	47.0%	53.0%
104882	473	3'-UTR	82.7%	17.3%
104883	474	3'-UTR	46.4%	53.6%
104884	475	3'-UTR	46.1%	53.9%
104885	476	3'-UTR	156.9%	---
104886	477	3'-UTR	102.4%	---
104887	478	3'-UTR	59.1%	40.9%

104888	479	3'-UTR	64.7%	35.3%
104889	480	3'-UTR	83.7%	16.3%
104890	481	3'-UTR	52.9%	47.1%
104891	482	3'-UTR	87.9%	12.1%
104892	483	3'-UTR	39.8%	60.2%
104893	484	3'-UTR	71.1%	28.9%
104894	485	3'-UTR	34.0%	66.0%
104895	486	3'-UTR	129.8%	---
104896	487	3'-UTR	57.6%	42.4%
104897	488	3'-UTR	49.6%	50.4%
104898	489	3'-UTR	71.7%	28.3%
104899	490	3'-UTR	101.5%	---
104900	491	3'-UTR	142.1%	---
104901	492	3'-UTR	55.9%	44.1%
104902	493	3'-UTR	85.3%	14.7%
104903	494	3'-UTR	46.0%	54.0%
104904	495	3'-UTR	59.9%	40.1%
104905	496	3'-UTR	47.2%	52.8%
104906	497	3'-UTR	56.3%	43.7%

Oligonucleotides 104662 (SEQ ID NO: 264), 104669 (SEQ ID NO: 271), 104670 (SEQ ID NO: 272), 104688 (SEQ ID NO: 290), 104695 (SEQ ID NO: 297), 104697 (SEQ ID NO: 299), 104713 (SEQ ID NO: 315), 104738 (SEQ ID NO:334), 104824 (SEQ ID NO: 418), 104826 (SEQ ID NO: 420), 104829 (SEQ ID NO: 423), 104831 (SEQ ID NO: 425), 104833 (SEQ ID NO: 427), 104837 (SEQ ID NO: 431), 104838 (SEQ ID NO: 432), 104841 (SEQ ID NO: 435), 104843 (SEQ ID NO: 437), 104844 (SEQ ID NO: 438), 104845 (SEQ ID NO: 439), 104847 (SEQ ID NO: 441), 104854 (SEQ ID NO: 23), 104857 (SEQ ID NO: 92), 104864 (SEQ ID NO: 455), 104866 (SEQ ID NO: 457), 104867 (SEQ ID NO: 458), 104869 (SEQ ID NO: 460), 104872 (SEQ ID NO: 463), 104874 (SEQ ID NO: 465), 104875 (SEQ ID NO: 466), 104877 (SEQ ID NO: 468), 104880 (SEQ ID NO: 471), 104881 (SEQ ID NO: 472), 104883 (SEQ ID NO: 474), 104884 (SEQ ID NO: 475), 104892 (SEQ ID NO: 483), 104894 (SEQ ID NO: 485), 104897 (SEQ ID NO: 488), 104903 (SEQ ID NO: 494) and 104905 (SEQ ID NO: 496) gave approximately 50% or greater reduction in TNF-α mRNA expression in this assay. Oligonucleotides 104713 (SEQ ID NO: 315), 104824 (SEQ ID NO: 418), 104833 (SEQ ID NO: 427), 104837 (SEQ ID NO: 431), 104838 (SEQ ID NO: 432), 104854 (SEQ ID NO: 23), 104857 (SEQ ID NO: 92), and 104869 (SEQ ID NO: 460) gave approximately 70% or greater reduction in TNF-α mRNA expression in this assay.

EXAMPLE 25: Dose response of chimeric (deoxy gapped) antisense phosphorothioate oligodeoxynucleotide effects on TNF-α mRNA and protein levels

Several oligonucleotides from the initial screen were chosen for dose response assays. NeoHk cells were grown, treated and processed as described in Example 3. LIPOFECTIN7 was added at a ratio of 3 μg/ml per 100 nM of oligonucleotide. The control included LIPOFECTIN7 at a concentration of 9 μg/ml.

The human promonocytic leukaemia cell line, THP-1 (American Type Culture Collection, Manassas, VA) was maintained in RPMI 1640 growth media supplemented with 10% fetal calf serum (FCS; Life Technologies, Rockville, MD).

A total of 8 x 10^5 cells were employed for each treatment by combining 50 µl of cell suspension in OPTIMEM™, 1% FBS with oligonucleotide at the indicated concentrations to reach a final volume of 100 µl with OPTIMEM™, 1% FBS. Cells were then transferred to a 1 mm electroporation cuvette and electroporated using an Electrocell Manipulator 600 instrument (Biotechnologies and Experimental Research, Inc.) employing 90 V, 1000 µF, at 13 Ω. Electroporated cells were then transferred to 24 well plates. 400 µl of RPMI 1640, 10% FCS was added to the cells and the cells were allowed to recover for 6 hrs. Cells were then induced with LPS at a final concentration of 100 ng/ml for 2 hours. RNA was isolated and processed as described in Example 3. Results with NeoHK cells are shown in Table 38 for mRNA, and Table 39 for protein. Results with THP-1 cells are shown in Table 40.

Most of the oligonucleotides tested showed dose response effects with a maximum inhibition of mRNA greater than 70% and a maximum inhibition of protein greater than 85%.

TABLE 38

Dose Response of NeoHK Cells to TNF-α
Chimeric (deoxy gapped) Antisense Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
induced	---	---	---	100%	---
16798	128	coding	30 nM	87%	13%
"	"	"	100 nM	129%	---
"	"	"	300 nM	156%	---
21823	69	intron 1	30 nM	82%	18%
"	"	"	100 nM	90%	10%
"	"	"	300 nM	59%	41%
28088	68	intron 1	30 nM	68%	32%
"	"	"	100 nM	43%	57%
"	"	"	300 nM	42%	58%

28089	69	intron 1	30 nM	59%	41%
"	"	"	100 nM	44%	56%
"	"	"	300 nM	38%	62%
104697	299	coding	30 nM	60%	40%
"	"	"	100 nM	45%	55%
"	"	"	300 nM	27%	73%
104777	372	3'-UTR	30 nM	66%	34%
"	"	"	100 nM	55%	45%
"	"	"	300 nM	43%	57%

TABLE 39

Dose Response of NeoHK Cells to TNF-α
Chimeric (deoxy gapped) Antisense Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% Protein Expression	% Protein Inhibition
induced	---	---	---	100.0%	---
16798	128	coding	30 nM	115.0%	---
"	"	"	100 nM	136.0%	---
"	"	"	300 nM	183.0%	---
28089	69	intron 1	30 nM	87.3%	12.7%
"	"	"	100 nM	47.4%	52.6%
"	"	"	300 nM	22.8%	77.2%
104681	283	coding	30 nM	91.3%	8.7%
"	"	"	100 nM	62.0%	38.0%
"	"	"	300 nM	28.5%	71.5%
104697	299	coding	30 nM	87.1%	12.9%
"	"	"	100 nM	59.6%	40.4%
"	"	"	300 nM	29.1%	70.9%
104838	432	coding	30 nM	91.9%	8.1%
"	"	"	100 nM	56.9%	43.1%
"	"	"	300 nM	14.8%	85.2%
104854	23	coding	30 nM	64.4%	35.6%
"	"	"	100 nM	42.3%	57.7%

"	"	"	300 nM	96.1%	3.9%
104869	460	3'-UTR	30 nM	88.9%	11.1%
"	"	"	100 nM	56.8%	43.2%
"	"	"	300 nM	42.3%	57.7%

TABLE 40

Dose Response of LPS-Induced THP-1 Cells to Chimeric (deoxy gapped) TNF-α Antisense Phosphorothioate Oligodeoxynucleotides (ASOs)

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
induced	---	---	---	100%	---
16798	128	coding	1 μM	102%	--
"	"	"	3 μM	87%	13%
"	"	"	10 μM	113%	---
"	"	"	30 μM	134%	---
28089	69	intron 1	1 μM	39%	61%
"	"	"	3 μM	79%	21%
"	"	"	10 μM	91%	9%
"	"	"	30 μM	63%	37%
104697	299	coding	1 μM	99%	1%
"	"	"	3 μM	96%	4%
"	"	"	10 μM	92%	8%
"	"	"	30 μM	52%	48%
104838	432	coding	1 μM	31%	69%
"	"	"	3 μM	20%	80%
"	"	"	10 μM	15%	85%
"	"	"	30 μM	7%	93%
104854	23	coding	1 μM	110%	---
"	"	"	3 μM	90%	10%
"	"	"	10 μM	95%	5%
"	"	"	30 μM	61%	39%

EXAMPLE 26: Further Optimization of Human TNF-α Antisense Oligonucleotide Chemistry

Additional analogs of TNF-α oligonucleotides were designed and synthesized to find an optimum gap size. The sequences and chemistries are shown in Table 36.

Dose response experiments are performed as described in Example 3.

TABLE 41

Nucleotide Sequences of TNF-α Chimeric Backbone (deoxy gapped) Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
110554	**GCTG**ATTAGAGAGA**GGTCCC**	432	104838 analog	
110555	**GCT**GATTAGAGAG**AGGTCCC**	"	"	
110556	**GC**TGATTAGAGA**GAGGTCCC**	"	"	
110557	**G**CTGATTAGAG**AGAGGTCCC**	"	"	
110583	GCTGATTAGA**GAGAGGTCCC**	"	"	
110558	**CTGA**TTAGAGAGAG**GTCCC**	498	1596-1614	coding
110559	**CTG**ATTAGAGAGAG**GTCCC**	"	"	"
110560	**CTG**ATTAGAGAGA**GGTCCC**	"	"	"
110561	**CT**GATTAGAGAGAG**GTCCC**	"	"	"
110562	**CT**GATTAGAGAGA**GGTCCC**	"	"	"
110563	**CT**GATTAGAGAG**AGGTCCC**	"	"	"
110564	**C**TGATTAGAGAGAG**GTCCC**	"	"	"
110565	**C**TGATTAGAGAGA**GGTCCC**	"	"	"
110566	**C**TGATTAGAGAG**AGGTCCC**	"	"	"
110567	**C**TGATTAGAGA**GAGGTCCC**	"	"	"
110584	CTGATTAGAG**AGAGGTCCC**	"	"	"
108371	**CTGA**TTAGAGAGAG**GTCC**	499	1597-1614	coding
110568	**CTG**ATTAGAGAGA**GGTCC**	"	"	"
110569	**CT**GATTAGAGAG**AGGTCC**	"	"	"

110570	CTGATTAGAGA**GAGGTCC**	"	"	"
110585	CTGATTAGAG**AGAGGTCC**	"	"	"
110571	**CTGGTTA**TCTCTCAGCT**CCA**	299	104697 analog	
110572	**CTGGTTAT**CTCTCAGCTC**CA**	"	"	
110573	**CTG**GTTATCTCTC**AGCTCCA**	"	"	
110586	CTGGTTATCT**CTCAGCTCCA**	"	"	
110574	**GATCACT**CCAAAGTGCA**GCA**	283	104681 analog	
110575	**GATCACTC**CAAAGTGCAG**CA**	"	"	
110576	**GAT**CACTCCAAAG**TGCAGCA**	"	"	
110587	GATCACTCCA**AAGTGCAGCA**	"	"	
110577	**AGCTTGG**GTTCCGACCC**TAA**	460	104689 analog	
110578	**AGCTTGGG**TTCCGACCCT**AA**	"	"	
110579	**AGC**TTGGGTTCCG**ACCCTAA**	"	"	
110588	AGCTTGGGTT**CCGACCCTAA**	"	"	
110580	**AGGTTGA**CCTTGGTCTG**GTA**	315	104713 analog	
110581	**AGGTTGAC**CTTGGTCTGG**TA**	"	"	
110582	**AGG**TTGACCTTGG**TCTGGTA**	"	"	
110589	AGGTTGACCT**TGGTCTGGTA**	"	"	
110637	**GTGTG**CCAGACACCC**TATCT**	69	21823 analog	
110651	**GTGT**GCCAGACACC**CTATCT**	"	"	
110665	**GTG**TGCCAGACAC**CCTATCT**	"	"	
110679	**GT**GTGCCAGACA**CCCTATCT**	"	"	
110693	**G**TGTGCCAGAC**ACCCTATCT**	"	"	
110707	GTGTGCCAGA**CACCCTATCT**	"	"	
110590	**TGAGT**GTCTTCTGTG**TGCCA**	500	1411-1430	intron 1
110597	**TGAG**TGTCTTCTGT**GTGCCA**	"	"	"
110604	**TGA**GTGTCTTCTG**TGTGCCA**	"	"	"
110611	**TG**AGTGTCTTCT**GTGTGCCA**	"	"	"
110618	**T**GAGTGTCTTC**TGTGTGCCA**	"	"	"
110625	TGAGTGTCTT**CTGTGTGCCA**	"	"	"
110591	**GAGTG**TCTTCTGTGT**GCCAG**	501	1410-1429	intron 1
110598	**GAGT**GTCTTCTGTG**TGCCAG**	"	"	"
110605	**GAG**TGTCTTCTGT**GTGCCAG**	"	"	"

110612	**GA**GTGTCTTCTG**TGTGCCAG**	"	"	"
110619	**G**AGTGTCTTCT**GTGTGCCAG**	"	"	"
110626	GAGTGTCTTC**TGTGTGCCAG**	"	"	"
110592	**AGTGT**CTTCTGTGTG**CCAGA**	144	100181 analog	
110599	**AGTG**TCTTCTGTGT**GCCAGA**	"	"	
110606	**AGT**GTCTTCTGTG**TGCCAGA**	"	"	
110613	**AG**TGTCTTCTGT**GTGCCAGA**	"	"	
110620	**A**GTGTCTTCTG**TGTGCCAGA**	"	"	
110627	AGTGTCTTCT**GTGTGCCAGA**	"	"	
110593	**GTGTC**TTCTGTGTGC**CAGAC**	145	100182 analog	
110600	**GTGT**CTTCTGTGTG**CCAGAC**	"	"	
110607	**GTG**TCTTCTGTGT**GCCAGAC**	"	"	
110614	**GT**GTCTTCTGTG**TGCCAGAC**	"	"	
110621	**G**TGTCTTCTGT**GTGCCAGAC**	"	"	
110628	GTGTCTTCTG**TGTGCCAGAC**	"	"	
110594	**TGTCT**TCTGTGTGCC**AGACA**	146	100183 analog	
110601	**TGTC**TTCTGTGTGC**CAGACA**	"	"	
110608	**TGT**CTTCTGTGTG**CCAGACA**	"	"	
110615	**TG**TCTTCTGTGT**GCCAGACA**	"	"	
110622	**T**GTCTTCTGTG**TGCCAGACA**	"	"	
110629	TGTCTTCTGT**GTGCCAGACA**	"	"	
110595	**GTCTT**CTGTGTGCCA**GACAC**	147	100184 analog	
110602	**GTCT**TCTGTGTGCC**AGACAC**	"	"	
110609	**GTC**TTCTGTGTGC**CAGACAC**	"	"	
110616	**GT**CTTCTGTGTG**CCAGACAC**	"	"	
110623	**G**TCTTCTGTGT**GCCAGACAC**	"	"	
110630	GTCTTCTGTG**TGCCAGACAC**	"	"	
110596	**TCTTC**TGTGTGCCAG**ACACC**	148	100185 analog	
110603	**TCTT**CTGTGTGCCA**GACACC**	"	"	
110610	**TCT**TCTGTGTGCC**AGACACC**	"	"	
110617	**TC**TTCTGTGTGC**CAGACACC**	"	"	
110624	**T**CTTCTGTGTG**CCAGACACC**	"	"	
110631	TCTTCTGTGT**GCCAGACACC**	"	"	

110632	**CTTCT**GTGTGCCAGA**CACCC**	149	100186 analog	
110646	**CTTC**TGTGTGCCAG**ACACCC**	"	"	
110660	**CTT**CTGTGTGCCA**GACACCC**	"	"	
110674	**CT**TCTGTGTGCC**AGACACCC**	"	"	
110688	**C**TTCTGTGTGC**CAGACACCC**	"	"	
110702	CTTCTGTGTG**CCAGACACCC**	"	"	
110633	**TTCTG**TGTGCCAGAC**ACCCT**	150	100187 analog	
110647	**TTCT**GTGTGCCAGA**CACCCT**	"	"	
110661	**TTC**TGTGTGCCAG**ACACCCT**	"	"	
110675	**TT**CTGTGTGCCA**GACACCCT**	"	"	
110689	**T**TCTGTGTGCC**AGACACCCT**	"	"	
110703	TTCTGTGTGC**CAGACACCCT**	"	"	
110634	**TCTGT**GTGCCAGACA**CCCTA**	151	100188 analog	
110648	**TCTG**TGTGCCAGAC**ACCCTA**	"	"	
110662	**TCT**GTGTGCCAGA**CACCCTA**	"	"	
110676	**TC**TGTGTGCCAG**ACACCCTA**	"	"	
110690	**T**CTGTGTGCCA**GACACCCTA**	"	"	
110704	TCTGTGTGCC**AGACACCCTA**	"	"	
110635	**CTGTG**TGCCAGACAC**CCTAT**	152	100189 analog	
110649	**CTGT**GTGCCAGACA**CCCTAT**	"	"	
110663	**CTG**TGTGCCAGAC**ACCCTAT**	"	"	
110677	**CT**GTGTGCCAGA**CACCCTAT**	"	"	
110691	**C**TGTGTGCCAG**ACACCCTAT**	"	"	
110705	CTGTGTGCCA**GACACCCTAT**	"	"	
110636	**TGTGT**GCCAGACACC**CTATC**	153	100190 analog	
110650	**TGTG**TGCCAGACAC**CCTATC**	"	"	
110664	**TGT**GTGCCAGACA**CCCTATC**	"	"	
110678	**TG**TGTGCCAGAC**ACCCTATC**	"	"	
110692	**T**GTGTGCCAGA**CACCCTATC**	"	"	
110706	TGTGTGCCAG**ACACCCTATC**	"	"	
110638	**TGTGC**CAGACACCCT**ATCTT**	154	100191 analog	
110652	**TGTG**CCAGACACCC**TATCTT**	"	"	
110666	**TGT**GCCAGACACC**CTATCTT**	"	"	

110680	**TG**TGCCAGACAC**CCTATCTT**	"	"	
110694	**T**GTGCCAGACA**CCCTATCTT**	"	"	
110708	TGTGCCAGAC**ACCCTATCTT**	"	"	
110639	**GTGCC**AGACACCCTA**TCTTC**	155	100192 analog	
110653	**GTGC**CAGACACCCT**ATCTTC**	"	"	
110667	**GTG**CCAGACACCC**TATCTTC**	"	"	
110681	**GT**GCCAGACACC**CTATCTTC**	"	"	
110695	**G**TGCCAGACAC**CCTATCTTC**	"	"	
110709	GTGCCAGACA**CCCTATCTTC**	"	"	
110640	**TGCCA**GACACCCTAT**CTTCT**	156	100193 analog	
110654	**TGCC**AGACACCCTA**TCTTCT**	"	"	
110668	**TGC**CAGACACCCT**ATCTTCT**	"	"	
110682	**TG**CCAGACACCC**TATCTTCT**	"	"	
110696	**T**GCCAGACACC**CTATCTTCT**	"	"	
110710	TGCCAGACAC**CCTATCTTCT**	"	"	
110641	**GCCAG**ACACCCTATC**TTCTT**	157	100194 analog	
110655	**GCCA**GACACCCTAT**CTTCTT**	"	"	
110669	**GCC**AGACACCCTA**TCTTCTT**	"	"	
110683	**GC**CAGACACCCT**ATCTTCTT**	"	"	
110697	**G**CCAGACACCC**TATCTTCTT**	"	"	
110711	GCCAGACACC**CTATCTTCTT**	"	"	
110642	**CCAGA**CACCCTATCT**TCTTC**	158	100195 analog	
110656	**CCAG**ACACCCTATC**TTCTTC**	"	"	
110670	**CCA**GACACCCTAT**CTTCTTC**	"	"	
110684	**CC**AGACACCCTA**TCTTCTTC**	"	"	
110698	**C**CAGACACCCT**ATCTTCTTC**	"	"	
110712	CCAGACACCC**TATCTTCTTC**	"	"	
110643	**CAGAC**ACCCTATCTT**CTTCT**	159	100196 analog	
110657	**CAGA**CACCCTATCT**TCTTCT**	"	"	
110671	**CAG**ACACCCTATC**TTCTTCT**	"	"	
110685	**CA**GACACCCTAT**CTTCTTCT**	"	"	
110699	**C**AGACACCCTA**TCTTCTTCT**	"	"	
110713	CAGACACCCT**ATCTTCTTCT**		"	

110644	**AGACA**CCCTATCTTC**TTCTC**	160	100197 analog	
110658	**AGAC**ACCCTATCTT**CTTCTC**	"	"	
110672	**AGA**CACCCTATCT**TCTTCTC**	"	"	
110686	**AG**ACACCCTATC**TTCTTCTC**	"	"	
110700	**A**GACACCCTAT**CTTCTTCTC**	"	"	
110714	AGACACCCTA**TCTTCTTCTC**	"	"	
110645	**GACAC**CCTATCTTCT**TCTCT**	161	100198 analog	
110659	**GACA**CCCTATCTTC**TTCTCT**	"	"	
110673	**GAC**ACCCTATCTT**CTTCTCT**	"	"	
110687	**GA**CACCCTATCT**TCTTCTCT**	"	"	
110701	**G**ACACCCTATC**TTCTTCTCT**	"	"	
110715	GACACCCTAT**CTTCTTCTCT**	"	"	

[1] Emboldened residues are 2'-methoxyethoxy residues (others are 2'-deoxy-). All 2'-methoxyethoxy cytidines and 2'-deoxycytidines are 5-methyl-cytidines; all linkages are phosphorothioate linkages.

[2]Co-ordinates from Genbank Accession No. X02910, locus name "HSTNFA", SEQ ID NO. 1.

EXAMPLE 26: Effect of TNF-α antisense oligonucleotides in TNF-α transgenic mouse models

The effect of TNF-α antisense oligonucleotides is studied in transgenic mouse models of human diseases. Such experiments can be performed through contract laboratories (e.g., The Laboratory of Molecular Genetics at The Hellenic Pasteur Institute, Athens, Greece) where such transgenic mouse models are available. Such models are available for testing human oligonucleotides in arthritis (Keffer, J., et al., *EMBO J.*, **1991**, *10*, 4025-4031) and multiple sclerosis (Akassoglou et al., *J. Immunol.*, **1997**, *158*, 438-445) models. A model for inflammatory bowel disease is available for testing mouse oligonucleotides (Kontoyiannis et al., *Immunity*, **1999**, *10*, 387-398).

Briefly, litters of the appropriate transgenic mouse strain are collected and weighed individually. Twice weekly from

birth, oligonucleotide in saline is administered intraperitoneally or intravenously. Injections continue for 7 weeks. Each week the animals are scored for manifestations of the appropriate disease. After the final treatment, the mice are sacrificed and histopathology is performed for indicators of disease as indicated in the references cited for each model.